

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 ; Search time 11.5 Seconds
(without alignments)
66.916 Million cell updates/sec

Title: VARIANT2
Perfect score: 25
Sequence: 1 XQXXVXHI 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 148

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: PIR 78:*
2: p1r1:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	52.0	8	2 A31570	angiotensin-conver
2	13	52.0	8	2 A61496	ubiquitin - celer
3	13	52.0	8	2 S53008	citrate synthase -
4	12	48.0	8	2 PT0368	Ig gamma chain C r
5	12	48.0	8	2 A42689	major postsynaptic
6	10	40.0	8	2 T14906	hypothetical prote
7	10	40.0	8	2 PH1618	Ig H chain V-D-J r
8	10	40.0	8	2 B47594	aspartate kinase (
9	9	36.0	8	2 XGHUEU	urine glycopeptide
10	9	36.0	8	2 S43971	tumor-associated a
11	9	36.0	8	2 S43972	tumor-associated a
12	9	36.0	8	2 T10077	hypothetical prote
13	9	36.0	8	2 S68802	nitrate reductase
14	9	36.0	8	2 PQ0726	unidentified 4.5/4
15	9	36.0	8	2 JS0316	leucokinin VI - Ma
16	9	36.0	8	2 B45800	serum albumin - do
17	9	36.0	8	2 A54823	olfactory receptor
18	9	36.0	8	2 B54823	olfactory receptor
19	9	36.0	8	2 S65381	cytochrome-c oxida
20	9	36.0	8	2 S69165	ferredoxin a2 - Ja
21	9	36.0	8	2 A25836	L-serine ammonia-1
22	9	32.0	8	2 B24749	neuropeptide B - b
23	8	32.0	8	2 S19288	acylase - Kluyvera
24	8	32.0	8	2 S70727	lipg protein - Shi
25	8	32.0	8	2 S63493	disintegrin sulf
26	8	32.0	8	2 PA0035	protein Q430039 -
27	8	32.0	8	2 T10952	hypothetical prote
28	8	32.0	8	2 S78036	ribosomal protein
29	8	32.0	8	2 PT0030	inulinase (EC 3.2.

30	8	32.0	8	2 PL0162	paramyosin - north
31	8	32.0	8	2 A46306	spasmodic toxin
32	8	32.0	8	2 A14683	aspartate transami
33	8	32.0	8	2 PT0298	Ig heavy chain CRD
34	8	32.0	8	2 PT0323	Ig heavy chain CRD
35	8	32.0	8	2 PN0043	phosphatidylethano
36	8	32.0	8	2 A19404	prealbumin - weste
37	8	32.0	8	2 C39690	neural cell adhesi
38	8	32.0	8	2 A35180	neutral proteinase
39	8	32.0	8	2 PC4372	telomeric and tetr
40	8	32.0	8	2 S29272	tocopherol-binding
41	7	28.0	8	2 A61348	red pigment-concen
42	7	28.0	8	2 A28004	adipokinetic hormo
43	7	28.0	8	2 S08995	hypertrehalosemic
44	7	28.0	8	2 S08996	hypertrehalosemic
45	7	28.0	8	2 S10596	adipokinetic hormo

ALIGNMENTS

RESULT 1
A31570
angiotensin-converting enzyme inhibitor - yellowfin tuna
C:Species: Thunnus albacares (yellowfin tuna)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000
C:Accession: A31570
R:Kohama, Y.; Matsunoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.
Biochem. Biophys. Res. Commun. 155, 332-337, 1988
A:Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.
A:Reference number: A31570; PMID:88326322; PMID:3415688
A:Accession: A31570
A:Molecule type: protein
A:Residues: 1-8 <KOH>
A:Note: the source is designated as Neorhynchus macropterus
C:Keyword: angiotensin-converting enzyme inhibitor

Query Match 52.0%; Score 13; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHI 8
DB 2 TH1 4

RESULT 2

A61496
ubiquitin - celer (fragment)
C:Species: Apium graveolens (celer)
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
C:Accession: A61496
R:Goldstein, G.; Scheid, M.; Hammerling, U.; Boyse, E.A.; Schlessinger, D.H.; Niall, H.D.
Proc. Natl. Acad. Sci. U.S.A. 72, 11-15, 1975
A:Title: Isolation of a polypeptide that has lymphocyte-differentiating properties and is
A:Reference number: A61496; PMID:75120426; PMID:1078892
A:Accession: A61496
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <GOL>
A:Note: a small amount of material was sequenced; the amino-terminal residue is unlikely

Query Match 52.0%; Score 13; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
DB 1 XQIXVK 6

RESULT 3

SS53008
 citrate synthase - cucurbit
 C:Species: Cucurbita sp. (cucurbit)
 C:Date: 14-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
 C:Accession: SS53008
 R:Rato, A.; Hayashi, M.; Mori, H.; Nishimura, M.
 Plant Mol. Biol. 27, 377-390, 1995
 A:Title: Molecular characterization of a glyoxysomal citrate synthase that is synthesized
 A:Reference number: SS53007; PMID:95195164; PMID:7888626
 A:Accession: SS53008
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <KAT>

Query Match 52.0%; Score 13; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 :|:|:
 Db 2 AQTMTVA 7

RESULT 4
 PT0368
 Ig gamma chain C region (gamma-1) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-1996
 C:Accession: PT0368
 R:Milli, M.; Fougereau, M.; Guglielmi, P.; Schiffr, C.
 Mol. Immunol. 28, 753-761, 1991
 A:Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.
 A:Reference number: PT0368; PMID:91312348; PMID:1906981
 A:Accession: PT0368
 A:Molecule type: mRNA
 A:Residues: 1-8 <MTL>
 A:Experimental source: fetal liver
 C:Keywords: immunoglobulin

Query Match 48.0%; Score 12; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 :|:|:
 Db 2 HQGPIC 7

RESULT 5
 A42689
 major postsynaptic density protein - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 26-May-1994
 C:Accession: A42689
 R:Mu, K.; Huang, Y.; Adler, J.; Black, I.B.
 Proc. Natl. Acad. Sci. U.S.A. 89, 3015-3019, 1992
 A:Title: On the identity of the major postsynaptic density protein.
 A:Reference number: A42689; PMID:92212958; PMID:1131576
 A:Accession: A42689
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <WUA>

Query Match 48.0%; Score 12; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHI 8
 :|:|:
 Db 2 LKVPNI 7

RESULT 6

T14906
 hypothetical protein - parsley
 C:Species: Petroselinum crispum (parsley)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T14906
 R:Feldbrugge, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Hatter, K.; Weishaar, B.
 Plant Cell 6, 1607-1621, 1994
 A:Title: Functional analysis of a light-responsive plant bZIP transcriptional regulator.
 A:Reference number: T14906; PMID:95128172; PMID:7827494
 A:Accession: T14906
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-8 <FTU>
 A:Cross-references: EMBL:575395; NID:9913201; PID:e194245

Query Match 40.0%; Score 10; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXXH 7
 :|:
 Db 1 MKH 3

RESULT 7
 PH1618
 Ig H chain V-D-J region (clone B-1ess 33) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1618
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; PMID:93301609; PMID:8315387
 A:Accession: PH1618
 A:Molecule type: DNA
 A:Residues: 1-8 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 40.0%; Score 10; DB 2; Length 8;
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 XVXH 7
 :|:
 Db 1 CARH 4

RESULT 8
 B47594
 aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)
 C:Species: Corynebacterium flavum
 C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997
 C:Accession: B47594
 R:Follettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.
 J. Bacteriol. 175, 4096-4103, 1993
 A:Title: Gene structure and expression of the Corynebacterium flavum N13 ask-ase operon.
 A:Reference number: A47594; PMID:93308089; PMID:8100567
 A:Accession: B47594
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-8 <FOU>
 C:Keywords: phosphotransferase

Query Match 40.0%; Score 10; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 :|:|:
 Db 1 MERAIVL 6

RESULT 9

XGHUEU
 urine glycopeptide - human
 C:Species: Homo sapiens (man)
 C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C/Accession: A03188
 R:Rote, C.J.; Weiss, J.B.
 Blochem. J. 123: 25P, 1971
 A>Title: Identification in urine of a low-molecular-weight polar glycopeptide containing
 A/Reference number: A03188; PMID:72062338; PMID:5126885
 A/Accession: A03188
 A/Molecule type: protein
 A/Residues: 1-8 <LOT>
 C/Comment: The identity of the glycoprotein from which this peptide is derived is unknown
 re has also been found (see PIR:XGHUE).
 C/Superfamily: unassigned animal peptides
 C/Keywords: glycoprotein
 F/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XX 7
 : : :
 Db 2 EH 3

RESULT 10

S43971
 tumor-associated antigen MUT1 - mouse
 C:Species: Mus musculus (house mouse)
 C/Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
 C/Accession: S43971
 R:Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
 Nature 369, 67-71, 1994
 A>Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine
 A/Reference number: S43971; PMID:94217811; PMID:8164742
 A/Accession: S43971
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-8 <MAN>
 C/Superfamily: unassigned animal peptides

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;

Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XXXXX 6
 : : : : :
 Db 2 EQNTAQ 7

RESULT 11

S43972
 tumor-associated antigen MUT2 - mouse
 C:Species: Mus musculus (house mouse)
 C/Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
 C/Accession: S43972
 R:Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
 Nature 369, 67-71, 1994
 A>Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine
 A/Reference number: S43971; PMID:94217811; PMID:8164742
 A/Accession: S43972
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-8 <MAN>
 C/Superfamily: unassigned animal peptides

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XXXXX 6
 : : : : :
 Db 2 EQNTAQ 7

RESULT 12

T10077
 hypothetical protein N - Methylophilus methylotrophus (fragment)
 C:Species: Methylophilus methylotrophus
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C/Accession: T10077
 R:Chistoserdov, A.V.; McIntire, W.S.; Mathews, F.S.; Lidstrom, M.E.
 J. Bacteriol. 176, 4073-4080, 1994
 A>Title: Organization of the methyamine utilization (man) genes in Methylophilus methylotrophus
 A/Reference number: Z16936; PMID:94224247; PMID:80211188
 A/Accession: T10077
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-8 <CHI>
 A/Cross-references: EMBL:L26407; NID:G561931; PID:AA646955.1; PID:G561933
 A/Experimental source: strain W3A1
 C/Genetics:
 A/Gene: manN

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 20.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXX 5
 : : : : :
 Db 4 LQAIL 8

RESULT 13

S68802
 nitrate reductase (NADH) inhibitor - spinach (fragment)
 C:Species: Spinacia oleracea (spinach)
 C/Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
 C/Accession: S68802
 R:Beckmann, M.; Huber, J.L.; Liao, P.C.; Gage, D.A.; Huber, S.C.
 FEBS Lett. 387, 127-131, 1996
 A>Title: The inhibitor protein of phosphorylated nitrate reductase from spinach (Spinach)
 A/Reference number: S68802; PMID:96244508; PMID:8674533
 A/Accession: S68802
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-8 <BAC>
 A/Experimental source: leaves; strain cv. Bloomsdale

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 20.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXXXX 7
 : : : : :
 Db 3 LSVAY 7

RESULT 14

PQ0726
 unidentified 4.5/45K (imported) - rice (fragment)
 C:Species: Oryza sativa (rice)
 C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C/Accession: PQ0726
 R:Komatsu, S.; Kajiwara, H.; Hirano, H.
 Theor. Appl. Genet. 86, 935-942, 1993
 A>Title: A rice protein library; a data-file of rice proteins separated by two-dimensional
 A/Reference number: PQ0696
 A/Accession: PQ0726
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-8 <KOM>

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XXXVX 6
 :|:::
 Db 2 VQDDAA 7

RESULT 15
 JS0316
 leucokinin VI - Madeira cockroach
 C/Species: Leucophaea maderae (Madeira cockroach)
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C/Accession: JS0316
 R/Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 27-30, 1987
 A/Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic
 A/Reference number: JS0315
 A/Accession: JS0316
 A/Molecule type: protein
 A/Residues: 1-8 <HOL>
 C/Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act
 C/Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F/8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7
 :|:
 Db 4 FH 5

RESULT 16
 B45800
 serum albumin - dog (fragment)
 C/Species: Canis lupus familiaris (dog)
 C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 31-Dec-1993
 C/Accession: B45800
 R/Carraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.
 J. Immunol. 143, 1680-1684, 1989
 A/Title: Structures of histamine-releasing peptides formed by the action of acid proteas
 A/Reference number: A45800; PMID:89341406; PMID:2474609
 A/Accession: B45800
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-8 <CAR>

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7
 :|:
 Db 4 RH 5

RESULT 17
 A54823
 olfactory receptor I7 - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C/Accession: A54823
 R/Chess, A.; Simon, I.; Cedar, H.; Axel, R.
 Cell 78, 823-834, 1994
 A/Title: Allelic inactivation regulates olfactory receptor gene expression.
 A/Reference number: A54823; PMID:94373818; PMID:8087849
 A/Accession: A54823
 A/Status: preliminary
 A/Molecule type: DNA

A/Residues: 1-8 <CHE>
 Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7
 :|:
 Db 5 NH 6

RESULT 18
 B54823
 olfactory receptor I7 - western wild mouse (fragment)
 C/Species: Mus spretus (western wild mouse)
 C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C/Accession: B54823
 R/Chess, A.; Simon, I.; Cedar, H.; Axel, R.
 Cell 78, 823-834, 1994
 A/Title: Allelic inactivation regulates olfactory receptor gene expression.
 A/Reference number: A54823; PMID:94373818; PMID:8087849
 A/Accession: B54823
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-8 <CHE>

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7
 :|:
 Db 5 NH 6

RESULT 19
 S65381
 cytochrome-c oxidase (EC 1.9.3.1) chain VIB, hepatic - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C/Accession: S65381
 R/Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
 Eur. J. Biochem. 230, 235-241, 1995
 A/Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-termi
 A/Reference number: S65372; PMID:95324529; PMID:7601105
 A/Accession: S65381
 A/Status: preliminary
 A/Molecule type: protein
 A/Molecule type: protein
 A/Residues: 1-8 <SCH>
 C/Keywords: oxidoreductase

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVX 6
 :|:::
 Db 1 QNXLD 5

RESULT 20
 S69165
 ferredoxin a2 - Japanese radish (fragment)
 C/Species: Kaiware daikon (Japanese radish)
 C/Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
 C/Accession: S69165
 R/Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
 Arch. Biochem. Biophys. 316, 797-802, 1995
 A/Title: Four ferredoxins from Japanese radish leaves.
 A/Reference number: S69164; PMID:95168667; PMID:7864635
 A/Accession: S69165
 A/Molecule type: protein
 A/Residues: 1-8 <OBA>

C;Keywords: 2pe-2s; electron transfer; iron-sulfur protein

Query Match 36.0%; Score 9; DB 2; Length 8;

Best Local Similarity 20.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXV 5

Db 4 EDDIV 8

RESULT 21

A25836

L-serine ammonia-lyase (EC 4.3.1.17) - Escherichia coli (fragment)

C;Species: Escherichia coli

C;Date: 24-Jan-1988 #sequence_revision 24-Jan-1988 #text_change 21-Jun-2002

C;Accession: A25836

R;Heinicz, M.C.; McFall, E.

J. Bacteriol. 123, 1163-1168, 1975

A;Title: N-terminal amino acid sequences of D-serine deaminases of wild-type and operat

A;Reference number: A25836; MUID:76005414; PMID:1059073

A;Contents: K12

A;Accession: A25836

A;Molecule type: protein

A;Residues: 1-8 <HEI>

C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; seri

Query Match 36.0%; Score 9; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7

Db 6 RH 7

RESULT 22

B24749

neuropeptide B - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000

C;Accession: B24749

R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.

A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two h

A;Reference number: A94074; MUID:86057985; PMID:3865193

A;Accession: B24749

A;Molecule type: protein

A;Residues: 1-8 <YAN>

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide

Query Match 32.0%; Score 8; DB 2; Length 8;

Best Local Similarity 25.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4

Db 3 FQPO 6

RESULT 23

S19288

acylase - Kluyvera cryocrescens

C;Species: Kluyvera cryocrescens

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C;Accession: S19288

R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Vidner, R.

Biochem. J. 280, 659-662, 1991

A;Title: Chemical modification of serine at the active site of penicillin acylase from K

A;Reference number: S19288; MUID:92109664; PMID:1764029

A;Accession: S19288

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <MAR>

Query Match 32.0%; Score 8; DB 2; Length 8;

Best Local Similarity 16.7%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXV 6

Db 1 CNMVI 6

RESULT 24

S70727

ipgf protein - Shigella flexneri (fragment)

C;Species: Shigella flexneri

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999

C;Accession: S70727

R;Allaoui, A.; Sansonetti, P.J.; Menard, R.; Barzu, S.; Mounier, J.; Phalipon, A.; Parsot

Mol. Microbiol. 17, 461-470, 1995

A;Title: Mxig, a membrane protein required for secretion of Shigella spp. Ipa invasins: j

A;Reference number: S70727; MUID:96100445; PMID:8559055

A;Accession: S70727

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-8 <ALT>

A;Cross-references: EMBL:Z48957; NID:9929880; PIDN:CA88821.1; PID:9929881

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995

C;Genetics: ipgf

Query Match 32.0%; Score 8; DB 2; Length 8;

Best Local Similarity 25.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4

Db 2 KONN 5

RESULT 25

S63493

dissimilatory sulfite reductase gamma chain, membrane-bound and soluble - Desulfovibrio c

C;Species: Desulfovibrio desulfuricans

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S63493; S63494

R;Staubert, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.

Eur. J. Biochem. 233, 873-879, 1995

A;Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio c

A;Reference number: S63489; MUID:96085152; PMID:8521853

A;Accession: S63493

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <ST2>

Query Match 32.0%; Score 8; DB 2; Length 8;

Best Local Similarity 0.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 0; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7

Db 1 ABITY 5

RESULT 26

PA0035

proteins QA300039 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997

C/Accession: PA0035
 R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 Submitted to JIPD, July 1994
 A/Description: Separation and characterization of Arabidopsis proteins by two-dimensional
 A/Reference number: PA0001
 A/Accession: PA0035
 A/Molecule type: protein
 A/Residues: 1-8 <KAM>
 A/Experimental source: stem

Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XQXX 4
 :||:
 Db 1 LQXD 4

RESULT 27
 T10952
 hypothetical protein 1 - spring vetch
 C/Species: Vicia sativa (spring vetch, tare)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C/Accession: T10952
 R/Christiansen, A.; Hansen, A.C.; Vijn, I.; Pallisgard, N.; Larsen, K.; Yang, W.C.; Blas
 submitted to the EMBL Data Library, December 1995
 A/Description: A novel type of DNA binding protein interacts with a conserved sequence
 A/Reference number: Z17228
 A/Accession: T10952
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 1-8 <CHR>
 A/Cross-references: EMBL:X95995; NID:G1360633; PID:e225824

Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 XQXXVX 6
 :||:
 Db 2 MMTLVS 7

RESULT 28
 S78036
 ribosomal protein Yns-B, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)
 C/Species: Saccharomyces cerevisiae
 C/Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
 C/Accession: S78036
 R/Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wiltma
 Eur. J. Biochem. 245, 449-456, 1997
 A/Title: Identification and characterization of the genes for mitochondrial ribosomal pr
 A/Reference number: S78018; MUID:97296414; PMID:9151978
 A/Accession: S78036
 A/Molecule type: protein
 A/Residues: 1-8 <KIT>
 A/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 :||:
 Db 1 MNXXVD 6

RESULT 29
 PT0030
 inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)
 N/Alternate names: inulase
 C/Species: Aspergillus ficuum

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999
 C/Accession: PT0030
 R/Ettalibi, M.; Baratti, J.C.
 Agric. Biol. Chem. 54, 61-68, 1990
 A/Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.
 A/Reference number: PT0030; MUID:90344234; PMID:1368526
 A/Accession: PT0030
 A/Molecule type: protein
 A/Residues: 1-8 <ETT>
 C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
 :||:
 Db 4 DQPY 7

RESULT 30
 PL0162
 paramyosin - northern quahog (fragment)
 C/Species: Mercenaria mercenaria (northern quahog)
 C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 11-May-2000
 C/Accession: PL0162
 R/Matabe, S.; Tsuchiya, T.; Hartshorne, D.J.
 Comp. Biochem. Physiol. B 94, 813-821, 1989
 A/Title: Phosphorylation of paramyosin.
 A/Reference number: PL0162; MUID:90107385; PMID:2532591
 A/Accession: PL0162
 A/Molecule type: protein
 A/Residues: 1-8 <MAT>
 A/Experimental source: white adductor muscle
 A/Note: the sequence is the phosphorylated tryptic peptide
 C/Comment: This protein is thought to exist as a dimer of two subunits, termed alpha-par
 om the carboxyl-terminal end of the molecule. Only alpha-paramyosin is phosphorylated by
 F;5/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 :||:
 Db 2 RSMVS 7

RESULT 31
 A46306
 spasmogenic toxin PNVI - spider (Phonetraxia nigriventer) (fragment)
 C/Species: Phonetraxia nigriventer
 C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
 C/Accession: A46306
 R/Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.C
 Toxicon 31, 377-384, 1993
 A/Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide
 A/Reference number: A46306; MUID:93276438; PMID:8503129
 A/Accession: A46306
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-8 <MAR>

Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
 :||:
 Db 5 GQST 8

RESULT 32

A14683

aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragment)

N/Alternate names: aspartate aminotransferase, mitochondrial

C/Species: Gallus gallus (chicken)

C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000

C/Accession: A14683

R/Wilson, K.J.; Hunziker, P.; Hughes, G.J.

PEBS Lett. 108, 98-102, 1979

A/Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.

A/Reference number: A14683; MUID:80092116; PMID:520566

A/Accession: A14683

A/Molecule type: Protein

A/Residues: 1-8 <MIL>

C/Keywords: aminotransferase; mitochondrion

Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;
Pred. No. 2.8e+05;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
:|:|:
Db 5 FQPK 8

RESULT 33

PT0298

Ig heavy chain CRD3 region (clone 5-103A) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0298

R/Yamada, M.; Maesselman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; MUID:91108337; PMID:1899102

A/Accession: PT0298

A/Molecule type: DNA

A/Residues: 1-8 <YAM>

A/Experimental source: B lymphocyte

C/Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;
Pred. No. 2.8e+05;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVX 6
:|:|:
Db 1 RMIVV 5

RESULT 34

PT0323

Ig heavy chain CRD3 region (clone J2-106B) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0323

R/Yamada, M.; Maesselman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; MUID:91108337; PMID:1899102

A/Accession: PT0323

A/Molecule type: DNA

A/Residues: 1-8 <YAM>

A/Experimental source: B lymphocyte

C/Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;
Pred. No. 2.8e+05;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
:|:|:
Db 4 GQRR 7

RESULT 35

PN0043

phosphatidylethanol amine-binding protein - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998

C/Accession: PN0043

R/Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A/Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro

A/Reference number: PN0041

A/Accession: PN0043

A/Molecule type: Protein

A/Residues: 1-8 <KAT>

A/Experimental source: neuroblastoma cell

C/Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is blocked.

C/Keywords: Brain

Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;
Pred. No. 2.8e+05;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
:|:|:
Db 3 EQLS 6

RESULT 36

I49404

prealbumin - western wild mouse (fragment)

C/Species: Mus spretus (western wild mouse)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C/Accession: I49404

R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.

Mamm. Genome 5, 349-355, 1994

A/Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A/Reference number: I49334; MUID:94319082; PMID:8043949

A/Accession: I49404

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-8 <RES>

A/Cross-references: EMBL:U05683; NID:9497008; PIDN:AAB60461.1; PID:G642825

Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;
Pred. No. 2.8e+05;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7
:|:|:
Db 1 AVVSN 5

RESULT 37

C39690

neural cell adhesion molecule, cardiac splice form - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999

C/Accession: C39690

R/Reyes, A.A.; Small, S.J.; Akesson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991

A/Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mR

A/Reference number: A39690; MUID:91141516; PMID:1996115

A/Accession: C39690

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar

A/Molecule type: mRNA

A/Residues: 1-8 <REY>

A/Cross-references: GB:M63970

C/Keywords: cardiac muscle; cell adhesion; heart

Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;
Pred. No. 2.8e+05;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXX 4
:|:|:
Db 3 VQGE 6

RESULT 38

A35180
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C/Accession: A35180
R/Yoshinaka, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Sato, M.
J. Biol. Chem. 265, 5809-5815, 1990
A/Title: Purification of a novel type of calcium-activated neutral protease from rat brain
A/Reference number: A35180, PMID:90202830; PMID:2318836
A/Accession: A35180
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-8 <YOS>
C/Keywords: hydrolase

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XQXXVX 6
:|:|:
Db 3 LSEGV 8

RESULT 39

PC4372
telomeric and tetraplex DNA binding protein qTPBP42 II - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C/Accession: PC4372
R/Saari, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A/Title: Telomeric and tetraplex DNA binding properties of qTPBP42: A homologue of the CA
A/Reference number: PC4371, PMID:97445086; PMID:9299414
A/Accession: PC4372
A/Molecule type: protein
A/Residues: 1-8 <SAR>
C/Comment: This protein binds either strand of the telomeric DNA as well as unimolecular
F.3-8/Domain: RNP2 #status predicted <RNP>

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXXVX 6
:|:|:
Db 1 KXRVG 5

RESULT 40

S29272
tocopherol-binding protein, 81k - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C/Accession: S29272
R/Nalecz, K.A.; Nalecz, M.J.; Azzi, A.
Eur. J. Biochem. 209, 37-42, 1992
A/Title: Isolation of tocopherol-binding proteins from the cytosol of smooth muscle A7-5
A/Reference number: S29272; PMID:93011150; PMID:1396710
A/Accession: S29272
A/Molecule type: protein
A/Residues: 1-8 <NAL>
A/Experimental source: smooth muscle A7-5 cells

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 XQXX 4
:|:|:
Db 4 DQXQ 7

RESULT 41

A61348
red pigment-concentrating hormone - northern shrimp
N/Alternate names: blanching hormone
C/Species: Penaeus borealis (northern shrimp)
C/Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C/Accession: A61348; S07139
R/Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A/Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A/Reference number: A61348, PMID:72228738; PMID:5041363
A/Accession: A61348
A/Molecule type: protein
A/Residues: 1-8 <FER1>
R/Fernlund, P.

Biochim. Biophys. Acta 371, 304-311, 1974
A/Title: Structure of the red-pigment-concentrating hormone of the shrimp, Penaeus borealis
A/Reference number: S07139; PMID:75054965; PMID:4433569
A/Accession: S07139
A/Molecule type: protein
A/Residues: 'E', 2-8 <FER2>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C/Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pig-
mented pigment-containing cells.
C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F.8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.0%; Score 7; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXX 4
:|:|:
Db 1 QLN 3

RESULT 42

A28004
adipokinetic hormone G - two-spotted cricket
N/Alternate names: AKH-G
C/Species: Gryllus bimaculatus (two-spotted cricket)
C/Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997
C/Accession: A28004
R/Gade, G.; Rinehart, K.L.
Biochem. Biophys. Res. Commun. 149, 908-914, 1987
A/Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptic
A/Reference number: A28004; PMID:88106553; PMID:3426616
A/Accession: A28004
A/Molecule type: protein
A/Residues: 1-8 <GAR>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F.8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.0%; Score 7; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXX 4
:|:|:
Db 1 QVN 3

RESULT 43

S08995

hypertrehalosemic hormone I - oriental cockroach

N/Alternate names: Pea-CAH-I

C/Species: Blatta orientalis (oriental cockroach)

C/Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997

C/Accession: S08995

R/Gade: G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entellae and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombard

A/Reference number: S08995; PMID:90253659; PMID:2340112

A/Accession: S08995

A/Molecule type: protein

A/Residues: 1-8 <GAE>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

28.0%; Score 7; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QVN 3

RESULT 44

S08996

hypertrehalosemic hormone II - oriental cockroach

N/Alternate names: Pea-CAH-II

C/Species: Blatta orientalis (oriental cockroach)

C/Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997

C/Accession: S08996

R/Gade: G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entellae and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombard

A/Reference number: S08995; PMID:90253659; PMID:2340112

A/Accession: S08996

A/Molecule type: protein

A/Residues: 1-8 <GAE>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

28.0%; Score 7; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QLT 3

RESULT 45

S10596

adipokinetic hormone - pond skimmer

C/Species: Libellula auripennis

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997

C/Accession: S10596

R/Gade: G.

Biol. Chem. Hoppe-Seyler 371, 475-483, 1990

A/Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating ho

A/Reference number: S10596; PMID:90359055; PMID:2390213

A/Accession: S10596

A/Molecule type: protein

A/Residues: 1-8 <BIO>

C/Comment: This peptide has both adipokinetic and hypertrehalosemic activities.

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

28.0%; Score 7; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QVN 3

Search completed: August 19, 2004, 15:51:22
Job time : 11.5 secs

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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 / Search time 8 Seconds

(without alignments)
52.070 Million cell updates/sec

Title: VARIANT2

Perfect score: 25
Sequence: 1 XQXVXHI 8

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	52.0	8	1 ACI_THUHL	P18691 thunnus alb
2	12	48.0	8	1 FUSO_FUSO	P81010 fusarium so
3	10	40.0	8	1 ANG2_BORJA	Q10582 bothrops ja
4	10	40.0	8	1 UPAL_HUMAN	P30087 homo sapien
5	9	36.0	8	1 ALIL_CYPPO	P82152 cydia pomon
6	9	36.0	8	1 COXG_RAT	P80430 rattus norv
7	9	36.0	8	1 GLUR_HUMAN	P02729 homo sapien
8	9	36.0	8	1 LCK4_LEUMA	P21143 leucophaea
9	9	36.0	8	1 LCK6_LEUMA	P19988 leucophaea
10	8	32.0	8	1 ACT_CARMA	P81820 carcinus ma
11	8	32.0	8	1 B44K_FORGI	P81866 porphyromon
12	8	32.0	8	1 CLP_THICU	P80488 chlobacilli
13	8	32.0	8	1 CPDI_ENTFA	P13269 enterococcu
14	8	32.0	8	1 LCK3_LEUMA	P21142 leucophaea
15	8	32.0	8	1 NPMB_BOVIN	P15507 bos taurus
16	8	32.0	8	1 UC26_MAIZE	P80632 zea mays (m
17	8	32.0	8	1 UF06_MOUSE	P36575 rattus norv
18	8	32.0	8	1 UH09_RAT	P36575 rattus norv
19	8	32.0	8	1 AKHG_GRYBI	P40868 gryllus bim
20	7	28.0	8	1 AKH_LIBAU	P25418 libellula a
21	7	28.0	8	1 AKH_MEML	P25423 melolontha
22	7	28.0	8	1 AKH_TABAT	P14555 tabanus atr
23	7	28.0	8	1 CADI_ENTFA	P13268 enterococcu
24	7	28.0	8	1 COM2_CONPU	P38785 cone purpu
25	7	28.0	8	1 HTF1_PERAM	P45458 periplaneta
26	7	28.0	8	1 HTF2_PERAM	P45459 periplaneta
27	7	28.0	8	1 HTP_TENNO	P25419 tenebrio mo
28	7	28.0	8	1 LPK_LEUMA	P13309 leucophaea
29	7	28.0	8	1 PLP_BRANA	P81707 brassica na
30	7	28.0	8	1 RPCH_PANBO	P80839 pandalis bo
31	7	28.0	8	1 VGLG_HSV2B	P81760 herpes simp
32	7	28.0	8	1 FARI_PENMO	P83316 penaeus mon
33	6	24.0	8	1	

34	6	24.0	8	1 FAR2_MACRS	P83275 macrobrachi
35	6	24.0	8	1 FAR3_HOMAM	P41486 homarus ame
36	6	24.0	8	1 FAR4_HOMAM	P41487 homarus ame
37	6	24.0	8	1 FAR7_ASCSU	P43171 ascaris suu
38	6	24.0	8	1 NSJ_MYCTU	P81152 mycobacteri
39	6	24.0	8	1 PPK3_PERAM	P82618 periplaneta
40	6	24.0	8	1 RT34_BOVIN	P82929 bos taurus
41	5	20.0	8	1 ALIL_CYPPO	P82157 cydia pomon
42	5	20.0	8	1 CCKN_MACEU	P30369 macropus eu
43	5	20.0	8	1 FAR4_MACSU	P83277 macrobrachi
44	5	20.0	8	1 FAR8_CALVO	P41863 calliphora
45	5	20.0	8	1 LMT2_LOCM1	P22396 locusta mig

ALIGNMENTS

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RESULT 1
ACI_THUHL          STANDARD;          PRT;          8 AA.
ID ACI_THUHL
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostei; Euteleostei;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
ON NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Minura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR; A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match          52.0%; Score 13; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHI 8
Db 2 THI 4

RESULT 2
FUSO_FUSO          STANDARD;          PRT;          8 AA.
ID FUSO_FUSO
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus s I3596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
ON NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RT Submitted (JUL-1997) to Swiss-Prot.
CC -!- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON TER
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

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Query Match 48.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 20.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7
 : : : :
 DB 1 TTM5H 5

RESULT 3

ANG2_BOTUA STANDARD; PRT; 8 AA.
 ID Q10562;
 AC Q10562;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide II (Fragment).
 OS Bothrops jararaca (Uroaraca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Bothrops.
 NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca."
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KM Vasconstrictor; Plasma; Serpin.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 40.0%; Score 10; DB 1; Length 8;
 Best Local Similarity 20.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
 : : : :
 DB 2 RYVYH 6

RESULT 4

UPAI_HUMAN STANDARD; PRT; 8 AA.
 ID UPAI_HUMAN
 AC P30087;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Fritiger S., Paquet N., Ravier F., Pasquall C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing."
 RT Electrophoresis 13:707-714(1992).
 RL Electrophoresis 13:707-714(1992).
 CC -1- FUNCTION: This protein is one of the determined pi of this unknown
 CC protein is: 4.9, its MW is: 65 kDa.
 DR SWISS-2DPAGE; P30087; HUMAN.
 FT NON TER 1
 FT UNSTRE 8
 FT NON_TER 8

SQ SEQUENCE 8 AA; 944 MW; C01772C455B80CDA CRC64;

Query Match 40.0%; Score 10; DB 1; Length 8;
 Best Local Similarity 16.7%; Pred. No. 1.4e+05;
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 : : : :
 DB 2 QESNVP 7

RESULT 5

AL11_CYPDO STANDARD; PRT; 8 AA.
 ID AL11_CYPDO
 AC P82152;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydia pomonella (Coddling moth).
 OS Cydia pomonella (Coddling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allostacin superfamily."
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: Belongs to the allostacin family.
 KM Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 36.0%; Score 9; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7
 : : : :
 DB 2 PH 3

RESULT 6

COXG_RAT STANDARD; PRT; 8 AA.
 ID COXG_RAT
 AC P80430;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIb (EC 1.9.3.1) (AED) (Fragment).
 GN COX6B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Mistar; TISSUE=Liver;
 RX MEDLINE=95324529; PubMed=7601105;
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
 RT amino-terminal sequences suggest identity of the fetal heart and the
 RT adult liver isoform."
 RL Eur. J. Biochem. 230:235-241(1995).
 CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
 CC chains of cytochrome c oxidase, the terminal oxidase in
 CC mitochondrial electron transport. This protein may be one of the
 CC heme-binding subunits of the oxidase.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome

CC C + 2 H(2)O.
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase VIB family.
 DR PIR: S65381; S65381.
 KM Oxidoreductase; Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1039 MW; 8101E9CAA73AE456 CRC64;
 Query Match 36.0%; Score 9; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QXXVX 6
 :|:|:
 Db 1 QNXLD 5

RESULT 7
 GLUR_HUMAN STANDARD; PRT; 8 AA.
 ID P02729;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urine glycopeptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72062338; PubMed=512685;
 RA Lote C.J., Weiss J.B.;
 RT "Identification in urine of a low-molecular-weight highly polar
 glycopeptide containing cysteinyl-galactose."
 RL Biochem. J. 123:25P-25P(1971).
 CC -1- FUNCTION: The identity of the glycoprotein from which this peptide
 is derived is unknown. No physiological function has been
 attributed. An erythrocyte membrane glycopeptide having a
 similar structure has also been found.
 CC PIR: A03188; XGHUED.
 DR GO; GO:0005576; C:extracellular; NMS.
 KM Glycoprotein.
 FT CARBOHYD 1 1
 SQ SEQUENCE 8 AA; 855 MW; C2D87A1F5B1EB1B CRC64;
 Query Match 36.0%; Score 9; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 XH 7
 :|:
 Db 2 EH 3

RESULT 8
 LCK4_LEUMA STANDARD; PRT; 8 AA.
 ID P21143;
 AC 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leucokinin IV (L-IV).
 OS Leucophaea maderae (Madella cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE. AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Primary structure and synthesis of two additional neuropeptides

RT from Leucophaea maderae: members of a new family of
 RT Cephalomyotropicins.";
 RL Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
 CC activity of cockroach proctodeum (hindgut).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 KM Neuropeptide; Amidation.
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA; 906 MW; DC635B1E9D5BDNA CRC64;
 Query Match 36.0%; Score 9; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 XH 7
 :|:
 Db 4 FH 5

RESULT 9
 LCK6_LEUMA STANDARD; PRT; 8 AA.
 ID P19988;
 AC 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leucokinin VI (L-VI).
 OS Leucophaea maderae (Madella cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RT TISSUE=Head;
 RX MEDLINE=87052651; PubMed=287794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 myotropic peptides of Leucophaea maderae."
 RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
 CC activity of cockroach proctodeum (hindgut).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR: JS0316; JS0316.
 KM Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1
 SQ SEQUENCE 8 AA; 935 MW; 9D635B1E9D5A5A6 CRC64;
 Query Match 36.0%; Score 9; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 XH 7
 :|:
 Db 4 FH 5

RESULT 10
 ACT_CARMA STANDARD; PRT; 8 AA.
 ID P80709;
 AC 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Actin (Fragment).
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.

RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
 RA Baghdasarian D.;
 RT "A. tranaololae. An enzyme implicated in crab steroidogenesis.";
 RL Endocrine 5:23-32(1996).
 CC -1- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
 CC 6.8, ITS MW IS: 46 KDa.
 CC -1- SIMILARITY: Belongs to the actin family.
 DR InterPro: IPR004000; Actin_like.
 DR PROSITE: PS00406; ACTINS_1; PARTIAL.
 DR PROSITE: PS00432; ACTINS_2; PARTIAL.
 DR PROSITE: PS01132; ACTINS_ACT LIKE; PARTIAL.
 KM Structural protein.
 FT NON_TER 1 8
 FT SEQUENCE 8 AA; 976 MW; 1424005AB2CAAB3 CRC64;
 SQ

Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 20.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVX 6
 DB 1 KCPVD 5

RESULT 11
 AL17_CARMA STANDARD; PRT; 8 AA.
 ID AL17_CARMA STANDARD; PRT; 8 AA.
 AC P81820;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Carcinus maenas (Common shore crab) (Green crab).
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OK NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 KM Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 8
 FT SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;
 SQ

Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QXX 4
 DB 2 QOXS 5

RESULT 12
 ID B44K_PORGI STANDARD; PRT; 8 AA.
 AC P81886;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 44 KDa immunogenic protein (Fragment).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OK NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VFB 3492;
 RX MEDLINE=20198497; PubMed=10731616;
 RA Norris J.M., Love D.N.;
 RT "Serum antibody responses of cats to soluble whole cell antigens of
 RT feline Porphyromonas gingivalis.";
 RL Vet. Microbiol. 73:37-49(2000).
 CC -1- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
 KM Antigen.
 FT NON_TER 8
 FT SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;
 SQ

Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QXX 4
 DB 3 YOKR 6

RESULT 13
 CLP_THICU STANDARD; PRT; 8 AA.
 ID CLP_THICU STANDARD; PRT; 8 AA.
 AC P80488;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE Chemolithotroph-specific protein (Fragment).
 OS Thiobacillus cuprinus.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Thiomonas.
 OK NCBI_TaxID=16860;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DSM 5494;
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
 RL Submitted (SEP-1995) to Swiss-Prot.
 CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
 CC CHEMOLITHOTROPHICALLY.
 FT NON_TER 8
 FT SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;
 SQ

Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QXX 4
 DB 4 AQEG 7

RESULT 14
 CPD1_ENTFA STANDARD; PRT; 8 AA.
 ID CPD1_ENTFA STANDARD; PRT; 8 AA.
 AC P13269;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CPD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OK NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85040388; PubMed=6436978;

RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B.;
 RT "Isolation and structure of bacterial sex pheromone, cpl1.",
 RL Science 226:849-850(1984).
 CC -1- FUNCTION: cpl1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC BACTERIOPHAGE PLASMID PP1.
 KM Pheromone.
 SQ SEQUENCE 8 AA; 913 MW; 86658729C682C729 CRC64;
 Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 16.7%; Pred. No. 1.4e+05;
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 XXVXHI 8
 Db 1 FVWFL 6

RESULT 15
 LCK3 LEUMA
 ID LCK3 LEUMA STANDARD; PRT; 8 AA.
 AC P21172;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leucokinin III (L-III).
 OS Leucophaea maderae (Madera cockroach).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Neoptera; Orthoptera; Dictyoptera; Blattaria; Blaberidae;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Primary structure and synthesis of two additional neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT Cephalomyotropins.";
 RL Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
 CC activity of cockroach proctodaeum (hindgut).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 KM Neuropeptide: Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;
 Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 XQXX 4
 Db 1 DQGF 4

RESULT 16
 NPMB BOVIN
 ID NPMB BOVIN STANDARD; PRT; 8 AA.
 AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Morphine modulating neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE=Brain;
 RX MEDLINE=86067985; PubMed=3865193;
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;

RT "Isolation, sequencing, synthesis, and pharmacological
 RT characterization of two brain neuropeptides that modulate the action
 RT of morphine.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
 CC -1- FUNCTION: Modulates the action of morphine.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR; B24749; B24749.
 KM Neuropeptide: Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;
 Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 XQXX 4
 Db 3 FQPD 6

RESULT 17
 UC26 MAIZE
 ID UC26 MAIZE STANDARD; PRT; 8 AA.
 AC P80632;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Penzance P., Riccardi F., Morin C., Damerval C., Huot J.-C.,
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 7.0, its MW is: 57.2 kDa.
 DR Maize-2DPRGS; P80632; COLEOPTILE.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;
 Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 XQXX 4
 Db 5 DQFK 8

RESULT 18
 UF06 MOUSE
 ID UF06 MOUSE STANDARD; PRT; 8 AA.
 AC P38644;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;

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RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Paterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -I- MISCELANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.2, its MW is: 50 kDa.
FT NON TER
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 H 7
DB 1 H 1

RESULT 19
UH09 RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Mistar; TISSUE=Heart;
RA Li X.-P., Pleisner K.-P., Scheeler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -I- MISCELANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 8.9, its MW is: 42 kDa.
FT NON TER
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXX 4
DB 4 R0SP 7

RESULT 20
AKHG GRYBI STANDARD; PRT; 8 AA.
AC P14066;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokine hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G. bimaculatus; TISSUE=Corpora cardiaca;
RA MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokine activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus.";
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RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R. microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilblsch C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -I- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4
DB 1 QVN 3

RESULT 21
AKH LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokine hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaepodera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokine/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -I- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR PIR: S10596; S10596.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4
DB 1 QVN 3
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Db 1 QVN 3

RESULT 22

AKH_MEMLT STANDARD; PRT; 8 AA.
 AC P25423;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone (AKH).
 OS Melolontha melolontha (Cockchafer),
 OS Geotrupes stercorarius (Dor beetle), and
 OS Pachnoda marginata (Flower beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;
 OC Scarabaeidae; Melolonthinae; Melolontha.
 NCBI_TaxID=7061, 7087, 7058;
 RX SPECIES=W.melolontha, and G.stercorarius; TISSUE=Corpora cardiaca;
 MEDLINE=91248100; PubMed=2039445;
 RA Gaede G.;
 RT "A unique charged tyrosine-containing member of the adipokinetic
 hormone/red-pigment-concentrating hormone peptide family isolated and
 sequenced from two beetle species."
 RL Biochem. J. 275:671-677(1991).
 RN
 RP SEQUENCE.
 RC SPECIES=E.marginata; TISSUE=Corpora cardiaca;
 MEDLINE=92265187; PubMed=1586453;
 RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
 RT "Primary structures of neuropeptides isolated from the corpora
 cardiaca of various cetonid beetle species determined by
 pulsed-liquid phase sequencing and tandem fast atom bombardment mass
 spectrometry."
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
 CC -1- FUNCTION: This hormone, released from cells in the corpora
 cardiaca after the beginning of flight, causes release of
 diglycerides from the fat body and then stimulates the flight
 muscles to use these diglycerides as an energy source.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPNH family.
 DR PIR: A58641; A58641.
 DR PIR: S15422; S15422.
 DR PIR: S21653; S21653.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;
 Query Match 28.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QXX 4
 DB 1 QLN 3
 RESULT 23
 AKH_TABAT STANDARD; PRT; 8 AA.
 AC P14595;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
 DE (DCC I).
 OC Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
 OC Tabanus.
 NCBI_TaxID=7207;
 RX SPECIES=T.abrassator; TISSUE=Corpora cardiaca;
 MEDLINE=90046758; PubMed=2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 hypotrehalosemic activity isolated from the corpora cardiaca of horse
 flies (Diptera)."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: This hormone, released from cells in the corpora
 cardiaca after the beginning of flight, causes release of
 diglycerides from the fat body and then stimulates the flight
 muscles to use these diglycerides as an energy source.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPNH family.
 DR PIR: A33995; A33995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 8678677A9D1A736 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QXX 4
 DB 1 QLT 3

RESULT 24

CAD1_ENTFA STANDARD; PRT; 8 AA.
 AC P13266;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Sex pheromone CAD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 NCBI_TaxID=1351;
 RN
 RP SEQUENCE.
 RX MEDLINE=85051889; PubMed=6437872;
 RA Mori M., Sakagami Y., Narita M., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B., Suzuki A.;
 RT "Isolation and structure of the bacterial sex pheromone, CAD1, that
 induces plasmid transfer in Streptococcus faecalis."
 RL FEMS Lett. 178:97-100(1994).
 CC -1- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PAD1.
 KW Pheromone.
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;
 Query Match 28.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 3 XXVX 6
 DB 3 SLVL 6
 RESULT 25
 COM2_CONPU STANDARD; PRT; 8 AA.
 AC P58785;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contrypphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxId=41690;
RN [1]
RP SEQUENCE. SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=9388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contrypphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -1- SIMILARITY: Belongs to the contrypphan family.
KM Toxin; Hydroxylation; D-amino acid.
FT DISUFID 2 8
FT MOD_RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;
OY 3 XXVX 6
Db 1 GCVL 4
Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Grylloblatta campodeiformis, Blattella germanica and Blattella orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is
CC the major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR PIR; A05169; A05169.
DR PIR; A44960; A44960.
DR PIR; A49823; A49823.
DR PIR; S08995; S08995.
DR InterPro; IPR02047; AKH.
DR PROSITE; PS00256; AKH; 1.
KM Neuropeptide; Amidation; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;
OY 2 QXX 4
Db 1 QVN 3
Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of *Periplaneta americana*.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [1]
RP SPECIES=L.deceimlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; Pubmed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; Pubmed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrichalosemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches *Leucophaea maderae*,
RT *Gromphadorhina portentosa*, *Blattella germanica* and *Blatta orientalis*
RT and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -1- FUNCTION: Hypertrichalosemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTM / RPCH family.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
DR Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
KM MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;
Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1,4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 2 QXX 4
DB 1 QLT 3
RESULT 28
HTF TENMO
ID HTF TENMO STANDARD; PRT; 8 AA.
AC P25419;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrichalosemic factor (HOTH) (Hypertrichalosemic neuropeptide).
OS Tenebrio molitor (yellow mealworm), and
OS Zophobas rugipes.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_Taxid=7067, 7075;
RN [1]
RP SPECIES=T.molitor, and Z.rugipes;
RX TISSUE=Corpora cardiaca;
RX MEDLINE=90341081; Pubmed=2381871;
RA Gaede G., Rosinski G.;
RT "The primary structure of the hypertrichalosemic neuropeptide from
RT tenebrionid beetles: a novel member of the AKH/RPCH family.";
RL Peptides 11:455-459(1990).
CC -1- FUNCTION: Hypertrichalosemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).

CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTM / RPCH family.
DR PIR; A43976; A43976.
DR PIR; B43976; B43976.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KM Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;
Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1,4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QXX 4
DB 1 QLN 3

RESULT 29
LPK LEUMA
ID LPK LEUMA STANDARD; PRT; 8 AA.
AC P13049;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 26-FEB-2003 (Rel. 41, Last annotation update)
DE Leukopyrokinin (LPK) (LBM-PK).
OS Leucophaea maderae (Maderia cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidae;
OC Blaberidae; Leucophaea.
OX NCBI_Taxid=6988;
RN [1]
RP SPECIES.
RX MEDLINE=86269041; Pubmed=3015140;
RA Nachman R.J., Holman G.M., Cook B.J.;
RT "Active fragments and analogs of the insect neuropeptide
RT leucopyrokinin: structure-function studies.";
RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
RN [2]
RP SPECIES, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=87052651; Pubmed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of a blocked myotropic
RT neuropeptide isolated from the cockroach, *Leucophaea maderae*.";
RL Comp. Biochem. Physiol. 85C:219-224(1986).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- MISCELLANEOUS: An analog without the N-terminal PCA residue was
CC synthesized and found to exhibit greater activity (1448) than the
CC parent neuropeptide. The portion of the sequence of LPK most
CC critical for the myotropic properties is limited to the
CC pentapeptide fragment FPRPL.
CC -1- SIMILARITY: Belongs to the pyrokinin family.
DR PIR; A23967; A23967.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KM Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;
Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1,4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 2 QXX 4
DB 1 QTS 3

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RESULT 30
PUP_BRANA STANDARD; PRT; 8 AA.
ID PUP_BRANA
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Placidal lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=706;
RN (1)
RP SEQUENCE.
RC STRAIN=CV, TOPAZ; TISSUE=Tapetum;
MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus."
RL Planta 208:588-596(1999).
CC -1- FUNCTION: May play a structural role in the elaioplast, a tapetum-
CC specific plastidial lipid organelle.
CC -1- TISSUE SPECIFICITY: Tapetum of anthers.
FT NON TER
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CMA042 CRC64;

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Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 5 VXHI 8
|:|
DB 1 VIDV 4

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RESULT 31
RPCH_PANBO STANDARD; PRT; 8 AA.
ID RPCH_PANBO
AC P08939;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Red pigment concentrating hormone (RPCH).
OS Pandanus borealis (Northern red shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidae;
OC Pandalidae; Pandalus.
NCBI_TaxID=6703;
RN (1)
RP SEQUENCE.
RX MEDLINE=75054965; PubMed=433569;
RA Fernlund P.;
RT "Structure of the red-pigment-concentrating hormone of the shrimp,
RT Pandalus borealis."
RL Biochim. Biophys. Acta 371:304-311(1974).
CC -1- FUNCTION: This hormone adapts the animal to light backgrounds by
CC stimulating concentration of the pigment of its red body-
CC chromatophores.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH: 1.
KW Pigment; Hormone; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 948 MW; 8678675B9C44736 CRC64;

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Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 2 QXX 4
|:|
DB 1 QLN 3

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RESULT 32
VGLG_HSV2B STANDARD; PRT; 8 AA.
ID VGLG_HSV2B
AC P81780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B43270R).
OS Varises; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=103921;
RN (1)
RP SEQUENCE.
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to Swiss-Prot.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GD, GI, AND GE.
CC -1- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
KW Glycoprotein.
FT NON TER
SQ SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;

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Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 3 XXVX 6
|:|
DB 2 SGVP 5

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RESULT 33
FARL_PENMO STANDARD; PRT; 8 AA.
ID FARL_PENMO
AC P83316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide Flrp (GDRNFRLR-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
NCBI_TaxID=6687;
RN (1)
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkaseem C., Longyant S.,
RA Chaivatsangkura P., Sithigorngul W., Peterson A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO: GO:0007218; P-neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1024 MW; 72D40729CA540XA8 CRC64;

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Query Match 24.0%; Score 6; DB 1; Length 8;
Best Local Similarity 0.0%; Pred. No. 1.4e+05;
Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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QY 1 XQXXVX 6 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

RESULT 34
 FAR2_MACRS STANDARD; PRT; 8 AA.

AC P41487;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE FMRamide-like neuropeptide FLP2 (ADNPLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonidae; Palaemonidae; Macrobrachium.
 NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE. AND MASS SPECTROMETRY.
 RC TISSUE=Byestalk;
 RA Stihgornigul P., Sarathongkum W., Jaldachoe S., Longyant S.,
 RA Stihgornigul W.,
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
 RT freshwater prawn Macrobrachium rosenbergii.";
 RL Comp. Biochem. Physiol. 120B:587-595 (1998).
 CC -1- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 DR GO:0007218; P:neuropeptide signaling pathway; TMS.
 KM Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 Db 2 DKNFLR 7

RESULT 35
 FAR3_HOMAM STANDARD; PRT; 8 AA.

AC P41486;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE FMRamide-like neuropeptide 3 (FLI 3) (F2).
 OS Homarus americanus (American lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Nephropoidea; Nephropoidea; Homarus.
 NCBI_TaxID=6706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=8811614; PubMed=3429714;
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
 RT "Purification and characterization of FMRamide-like immunoreactive
 RT substances from the lobster nervous system: Isolation and sequence
 RT analysis of two closely related peptides.";
 RL J. Comp. Neurol. 266:16-26 (1987).
 CC -1- MISCELLANEOUS: Pericardial organs release this peptide with 100 nm
 CC potassium in the presence of calcium.
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 KM Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

RESULT 36
 FAR4_HOMAM STANDARD; PRT; 8 AA.

AC P41487;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE FMRamide-like neuropeptide 4 (FLI 4) (F1).
 OS Homarus americanus (American lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Nephropoidea; Nephropoidea; Homarus.
 NCBI_TaxID=6706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=8811614; PubMed=3429714;
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
 RT "Purification and characterization of FMRamide-like immunoreactive
 RT substances from the lobster nervous system: Isolation and sequence
 RT analysis of two closely related peptides.";
 RL J. Comp. Neurol. 266:16-26 (1987).
 CC -1- FUNCTION: Can act as a modulator of exoskeletal and cardiac
 CC neuromuscular junctions.
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 KM Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 Db 2 NRNPLR 7

RESULT 37
 FAR7_ASCSU STANDARD; PRT; 8 AA.

AC P41471;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE FMRamide-like neuropeptide AF7.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
 OC Ascaridoidea; Ascaris.
 NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95380362; PubMed=7651904;
 RA Cowden C., Stretton A.O.W.;
 RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
 RT Ascaris suum.";
 RL Peptides 16:491-500 (1995).
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 KM Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6
 DB 4 RFLR 7

RESULT 38
 NS3_MYCTU STANDARD; PRT; 8 AA.

AC P8152;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30 kDa non-secretory protein 3 (Fragment).
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Corynebacteriinae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=H37Rv;
 RA Prasad H.K., Annapurna P.S.;
 RL Submitted (DEC-1997) to Swiss-Prot.
 CC -1- CAUTION: We are unable to find this protein in the translation of
 the genome of strain H37Rv.
 FT NON_TER 1 8
 FT NON_TER 1 8
 SQ SEQUENCE 8 AA; 919 MW; 8D3DC40B19CDD2D2 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 XXVX 6
 DB 1 VVA 3

RESULT 39
 PPK3_PERAM STANDARD; PRT; 8 AA.
 AC P82618;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FXPRU-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nechman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 abdominal neuromal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRUamides in the nervous system of
 the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 activity).
 CC -1- TISSUE SPECIFICITY: Corpora cardiaca.

CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
 CC -1- SIMILARITY: Belongs to the pyrokinin family.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 XXVX 6
 DB 1 LVP 3

RESULT 40
 RT34_BOVIN STANDARD; PRT; 8 AA.

AC P82929;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).
 GN MRPS34.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=21276436; PubMed=11279123;
 RA Koc B.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
 RT "The small subunit of the mammalian mitochondrial ribosome:
 identification of the full complement of ribosomal proteins present.";
 RL J. Biol. Chem. 276:19363-19374(2001).
 CC -1- SUBUNIT: Component of the mitochondrial ribosome small subunit
 (28S) which comprises a 12S rRNA and about 30 distinct proteins.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1 8
 FT NON_TER 1 8
 SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6
 DB 2 WGI 5

RESULT 41
 ALL6_CYDPO STANDARD; PRT; 8 AA.
 AC P82157;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydia pomonella (Coddling moth).
 OS Cydia pomonella (Coddling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Dive H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 Davey M., East P.D., Thorpe A.;

RT "lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 KM Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;
 Query Match 20.0%; Score 5; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7
 DB 1 LPLYN 5

RESULT 42
 CCKN_MACEU STANDARD; PRT; 8 AA.
 ID CCKN_MACEU
 AC P30369;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cholecystokinin (CCK).
 GN CCK.
 OS Macropus eugenii (Tamar wallaby), and
 OS Dasypus viverrinus (southeastern quoll).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9315, 9279;
 [1]
 RP SEQUENCE.
 RC SPECIES=M. eugenii, and D. viverrinus;
 RC TISSUE=Brain;
 RX MEDLINE=88234141; PubMed=3375140;
 RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
 RT "Cholecystokinin octapeptide purified from brains of Australian
 RT marsupials";
 RL Peptides 9:429-431(1988).
 CC -1- FUNCTION: This peptide hormone induces gall bladder contraction
 CC and the release of pancreatic enzymes in the gut. Its function in
 CC the brain is not clear.
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR PIR: A43001; A43001.
 DR PIR: PQ0012; PQ0012.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; GASTRIN; 1.
 KM Amidation; Sulfation; Hormone.
 FT MOD_RES 2
 FT MOD_RES 8
 FT MOD_RES 2
 SQ SEQUENCE 8 AA; 1064 MW; DDCA68378768B5A CRC64;
 Query Match 20.0%; Score 5; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 DB 2 YMGWMD 7

RESULT 43
 PAR4_MACRS STANDARD; PRT; 8 AA.
 ID PAR4_MACRS
 AC P83277;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLP4 (APALRFP-amide).
 OS Macrobrachium rosenbergii (Giant Fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.

OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Byestalk;
 RA Stihgornigul P.; Sarathongkum W., Jaidechoey S., Longyant S.,
 RA Stihgornigul W.;
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
 RT freshwater prawn Macrobrachium rosenbergii.";
 RL Comp. Biochem. Physiol. 120B:587-595 (1998).
 CC -1- MASS SPECTROMETRY: MW=943; METHOD=MALDI.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR GO: GO:0007218; P:neuropeptide signaling pathway; TAS.
 DE Neuropeptide; Amidation.
 FT MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 943 MW; 9CD40734072DC76D CRC64;
 Query Match 20.0%; Score 5; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 XXVXH 8
 DB 1 APALRL 6

RESULT 44
 PAR8_CALVO STANDARD; PRT; 8 AA.
 ID PAR8_CALVO
 AC P41863;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Calliphora vomitoria (Blue blowfly).
 OS Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=9219611; PubMed=1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliphorin) from the blowfly
 RT Calliphora vomitoria";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR PIR: H41978; H41978.
 DR Neuropeptide; Amidation.
 FT MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 957 MW; 72D4069C4A44DD8 CRC64;
 Query Match 20.0%; Score 5; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 DB 2 ANDPFR 7

RESULT 45
 LMT2_LOCM1 STANDARD; PRT; 8 AA.
 ID LMT2_LOCM1
 AC P22356;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-AUG-1991 (Rel. 19, Last annotation update)
 DE Locustamyotropin 2 (LOM-MT-2).

OS Locusta migratoria (migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin II, an
RT additional neuropeptide of Locusta migratoria. Member of the
RT cephalomyotropic peptide family.";
RL Insect Biochem. 20:479-484(1990).
CC -I- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -I- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 934 MW; 2634171A9CNA87B CRC64;

Query Match 20.0%; Score 5; DB 1; Length 8;
Best Local Similarity 0.0%; Pred. No. 1.4e+05;
Matches 0; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 XXVXHI 8
 :::;
Db 3 DFTPRL 8

Search completed: August 19, 2004, 15:51:49
Job time : 9 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 ; Search time 31 Seconds
(without alignments)
81.424 Million cell updates/sec

Title: VARIANT2
Perfect score: 25
Sequence: 1 XQXXVXHI 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 414

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	60.0	8	4	Q7Z6G0
2	14	56.0	8	2	Q56246
3	14	56.0	8	9	Q37854
4	14	56.0	8	13	Q91098
5	14	56.0	8	13	Q90498
6	13	52.0	8	2	P72279
7	13	52.0	8	2	P83152
8	12	48.0	8	5	Q9ZEW6
9	12	48.0	8	5	Q9ZEW6
10	12	48.0	8	5	Q9ZEW6
11	12	48.0	8	4	Q15894
12	11	44.0	8	4	Q9UWC7
13	11	44.0	8	6	Q9XSY1
14	11	44.0	8	8	Q8WGC9
15	11	44.0	8	8	Q8WGC9
16	11	44.0	8	10	Q8L802

17	11	44.0	8	13	P79940	P79940 xenopus lae
18	10	40.0	8	2	Q45615	Q45615 bacillus su
19	10	40.0	8	2	Q95443	Q95443 pseudomonas
20	10	40.0	8	2	Q8G340	Q8G340 borrelia bu
21	10	40.0	8	3	Q05403	Q05403 saccharomyc
22	10	40.0	8	3	Q13591	Q13591 saccharomyc
23	10	40.0	8	4	Q9BYV5	Q9BYV5 homo sapien
24	10	40.0	8	4	Q9UD24	Q9UD24 homo sapien
25	10	40.0	8	4	Q15893	Q15893 homo sapien
26	10	40.0	8	4	Q9UMH9	Q9UMH9 homo sapien
27	10	40.0	8	4	Q8IV87	Q8IV87 homo sapien
28	10	40.0	8	5	Q8MUN6	Q8MUN6 heliconius
29	10	40.0	8	5	Q86B59	Q86B59 strongyloce
30	10	40.0	8	6	Q9T778	Q9T778 canis fami
31	10	40.0	8	6	Q9BFR2	Q9BFR2 ursus arcto
32	10	40.0	8	6	Q9BFR2	Q9BFR2 macropus eu
33	10	40.0	8	6	Q9BFR0	Q9BFR0 trageleaphus
34	10	40.0	8	6	Q9BFR1	Q9BFR1 echinops te
35	10	40.0	8	6	Q9BFR1	Q9BFR1 ateleus fusc
36	10	40.0	8	6	Q9BFR7	Q9BFR7 caprine ind
37	10	40.0	8	6	Q9BFR9	Q9BFR9 euphractus
38	10	40.0	8	6	Q9BFR8	Q9BFR8 chaetophrac
39	10	40.0	8	6	Q9BFR0	Q9BFR0 macaca mula
40	10	40.0	8	6	Q9BFR8	Q9BFR8 loxodonta a
41	10	40.0	8	6	Q9BFR9	Q9BFR9 procavia ca
42	10	40.0	8	6	Q9BFR2	Q9BFR2 sorex arane
43	10	40.0	8	6	Q9BFR5	Q9BFR5 erinaceus c
44	10	40.0	8	6	Q9BFR6	Q9BFR6 myrmecophag
45	10	40.0	8	6	Q9BFR3	Q9BFR3 condylura c

ALIGNMENTS

RESULT 1	ID	Q7Z6G0	PRELIMINARY;	PRT;	8 AA.
AC	Q7Z6G0	Q7Z6G0			
DT	01-OCT-2003	(TREMBlrel. 25, Created)			
DT	01-OCT-2003	(TREMBlrel. 25, Last sequence update)			
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)			
DE	Fumarate hydratase (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Wei M.-H., Nickerson M.L., Toro J.R.;				
RT	"dinucleotide repeat polymorphisms in the fumarate hydratase gene of				
RL	human chromosome 1q42.3."				
DR	Submitted (May-2003) to the EMBL/GenBank/DBJ databases.				
FT	EMBL; AY29638; AAP5732.1;				
FT	NON_TER 1				
FT	NON_TER 8				
FT	NON_TER 8				
SO	SEQUENCE 8 AA; 881 MW; 40C5B1E732C44330 CRC64;				
Query Match	Score 15; DB 4; Length 8;				
Best Local Similarity	40.0%;				
Matches	2; Conservative				
	3; Mismatches				
	0; Indels				
	0; Gaps				
	0;				
QY	3 XXVXH 7				
DB	2 KXVLH 6				
RESULT 2	ID	Q56246	PRELIMINARY;	PRT;	8 AA.
AC	Q56246	Q56246			
DT	01-NOV-1996	(TREMBlrel. 01, Created)			
DT	01-JAN-1998	(TREMBlrel. 05, Last sequence update)			
DT	01-NOV-1998	(TREMBlrel. 08, Last annotation update)			

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DE Thermophilic proton ATPase epsilon subunit amino terminal (Fragment).
OS thermophilic bacterium PS3.
OC Bacteria; Firmicutes; Bacillales.
OX NCBI_TaxID=2334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PS3;
RX MEDLINE=87137359; PubMed=2880841;
RA Kagawa Y., Ishizuka M., Saitou T., Nakao S.;
RT "Stable structure of thermophilic proton ATPase beta subunit.";
RL J. Biochem. 100:923-934(1986).
DR EMBL; D00113; BAA00067.1; -.
DR EMBL; X04609; CAA28278.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 914 MW; EBD5A2C1E041A336 CRC64;

Query Match 56.0%; Score 14; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXHI 8
Db 1 MKTIHV 6

RESULT 3
Q37854 PRELIMINARY; PRT; 8 AA.
ID Q37854;
AC Q37854;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Coliphage gene of unknown function, 5' end (Fragment).
OS Bacteriophage R17.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OX NCBI_TaxID=12026;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=73224987; PubMed=4352721;
RA Rensing U.F.E.;
RT "A sequence of seventy-three nucleotides from the Coliphage R17
genome.";
RL Biochem. J. 131:593-604(1973).
DR EMBL; M24820; AAA72755.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 969 MW; ECB45412C1E72726 CRC64;

Query Match 56.0%; Score 14; DB 9; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 XVXHI 8
Db 1 MLTIHV 5

RESULT 4
Q91098 PRELIMINARY; PRT; 8 AA.
ID Q91098;
AC Q91098;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
DE Myoglobin (Fragment).
OS Manotina melanocephala (Noisy miner).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Meliphagidae; Manotina.
OX NCBI_TaxID=44314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D02;
RX MEDLINE=98208049; PubMed=9548272;

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RA Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;
RT "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae
RT assessed by temperature gradient gel electrophoresis.";
RL Electrophoresis 19:142-151(1998).
DR EMBL; U40497; AAC60364.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 890 MW; C6C1F2C865B046DE CRC64;

Query Match 56.0%; Score 14; DB 13; Length 8;
Best Local Similarity 28.6%; Pred. No. 1e+06;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXVXH 7
Db 1 CQISGVH 7

RESULT 5
Q90498 PRELIMINARY; PRT; 8 AA.
ID Q90498;
AC Q90498;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
DE Myoglobin (Fragment).
OS Erythrura gouldiae (Gouldian finch).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidae; Passeridae;
OC Erythrura.
OX NCBI_TaxID=44316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98208049; PubMed=9548272;
RA Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;
RT "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae
RT assessed by temperature gradient gel electrophoresis.";
RL Electrophoresis 19:142-151(1998).
DR EMBL; U40496; AAC60363.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 890 MW; C6C1F2C865B046DE CRC64;

Query Match 56.0%; Score 14; DB 13; Length 8;
Best Local Similarity 28.6%; Pred. No. 1e+06;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXVXH 7
Db 1 CQISGVH 7

RESULT 6
P72279 PRELIMINARY; PRT; 8 AA.
ID P72279;
AC P72279;
DT 01-FEB-1997 (T-EMBLrel. 02, Created)
DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Biphényl dioxygenase (Fragment).
OS Rhodococcus globenulus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriinae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=33008;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255652; PubMed=7737502;
RA Asturias J.A., Diaz B., Timmis K.N.;
RT "Evolutionary relationship of the biphényl dioxygenase of the gram-
RT positive bacterium Rhodococcus globenulus P6 to multicomponent
dioxygenases of gram-negative bacteria.";

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RL Gene 156:11-18(1995).
 DR EMBL; X80041; CA56350.1; -
 DR GO: GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
 KM Dioxigenase.
 PT NON_TER
 SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;
 Query Match 52.0%; Score 13; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XQXXVX 6
 DB 3 LQDEVV 8
 RESULT 7
 ID P83152 PRELIMINARY; PRT; 8 AA.
 AC P83152;
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Allophycocyanin beta chain (Fragment).
 OS Anabaena sp. (strain J31).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 NC NCB1_TaxID=29412;
 RN [1]
 RP SEQUENCE.
 RA Appte S.K., Uhlemann E., Schmid R., Alenddorf K.;
 RL Submitted (OCT-2001) to Swiss-Prot.
 CC -1- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
 FROM THE PHYCOBILIPROTEIN COMPLEX. ALLOPHYCOCYANIN HAS A MAXIMUM
 ABSORPTION AT APPROXIMATELY 650 TO 653 NANOMETERS.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.
 CC -1- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0030089; C:phycobillosome; IEA.
 DR GO: GO:0009579; C:chylakoid; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR GO: GO:0015979; P:photosynthesis; IEA.
 KM Phycobillosome; Electron transport; Photosynthesis; Bile pigment;
 KM Thylakoid; Membrane.
 PT NON_TER
 SQ SEQUENCE 8 AA; 788 MW; 87CDC1A05DDAB6DD CRC64;
 Query Match 52.0%; Score 13; DB 2; Length 8;
 Best Local Similarity 12.5%; Pred. No. 1e+06;
 Matches 1; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 1 XQXXVXH 8
 DB 1 AQDAITAV 8
 RESULT 8
 ID Q9ZE29 PRELIMINARY; PRT; 8 AA.
 AC Q9ZE29;
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
 GN LEUA.
 OS Buchnera aphidicola.
 OC Bacteri; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 NC NCB1_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99028904; PubMed=9812361;

RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
 RT "Structure and evolution of the leucine plasmids carried by the
 RT endosymbiont (Buchnera aphidicola) from aphids of the family
 RT Aphididae".
 RL FEMS Microbiol. Lett. 168:43-49(1998).
 DR EMBL; A0006874; CA007290.1; -
 DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO: GO:0003852; F:2-isopropylmalate synthase activity; IEA.
 DR GO: GO:0016829; P:lyase activity; IEA.
 KM lyase; Plasmid.
 PT NON_TER
 SQ SEQUENCE 8 AA; 917 MW; FE205042D6C5B446 CRC64;
 Query Match 48.0%; Score 12; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 1e+06;
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XQXXVX 6
 DB 3 SOVITL 8
 RESULT 9
 ID Q9TWH6 PRELIMINARY; PRT; 8 AA.
 AC Q9TWH6;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
 DE BIOACTIVE peptide P4=PUTATIVE ESOPHAGEAL NEUROREGULATOR.
 OS Perinereis vancaurica.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;
 OC Phyllodoctida; Nereididae; Perinereis.
 NC NCB1_TaxID=6355;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=95323338; PubMed=7599979;
 RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,
 RA Fujita T., Minkata H., Nomoto K.;
 RT "Isolation and characterization of four novel bioactive peptides from
 RT a polychaete annelid, Perinereis vancaurica".
 RL Comp. Biochem. Physiol. C, Pharmacol. Toxicol. Endocrinol. 110:297-
 RL 304(1995).
 SQ SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;
 Query Match 48.0%; Score 12; DB 5; Length 8;
 Best Local Similarity 14.3%; Pred. No. 1e+06;
 Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XQXXVXH 7
 DB 2 YEGDVPV 8
 RESULT 10
 ID O02032 PRELIMINARY; PRT; 8 AA.
 AC O02032;
 DT 01-JUL-1997 (T-EMBLrel. 04, Created)
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
 DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
 DE Metallothionein (Fragment).
 GN LPM2.
 OS Lytechinus pictus (Painted sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Metazoa; Echinodermata; Echinodermata; Temnopneustidae;
 OC Lytechinus.
 NC NCB1_TaxID=7653;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97264487; PubMed=9110313;
 RA Caerjesi P., Fang H., Brandhorst B.P.;
 RT "Metallothionein gene expression in embryos of the sea urchin

RT Lytechinus pictus.";
 RL Mol. Reprod. Dev. 47:39-46(1997).
 DR EMBL; Reprod. Dev. 47:39-46(1997).
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 823 MW; EBD5A2C1F7686766 CRC64;

Query Match 48.0%; Score 12; DB 5; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHX 8
 :|:
 Db 4 PHV 6

RESULT 11

Q34909 PRELIMINARY; PRT; 8 AA.
 AC Q34909;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome b (Fragment).
 OS Locusta migratoria (Migratory locust).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OC NCBI_TaxID=7004;

RP SEQUENCE FROM N.A.
 RX MEDLINE=88223478; PubMed=2836084;
 RA McCracken A., Uhlenbusch I., Gellissen G.;
 RT "Structure of the cloned locusta migratoria mitochondrial genome:
 RT restriction mapping and sequence of its ND-1 (URF-1) gene.";
 RL Curr. Genet. 11:625-630(1987).
 DR EMBL; X05286; CAA28905.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 48.0%; Score 12; DB 8; Length 8;
 Best Local Similarity 20.0%; Pred. No. 1e+06;
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7
 :|:
 Db 4 IKLKH 8

RESULT 12
 Q15894 PRELIMINARY; PRT; 8 AA.
 ID Q15894;
 AC Q15894;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE (Clone XP587B) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsey B.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries.";
 RL Hum. Mol. Genet. 0:0-0(1995).

DR EMBL; L32074; AAA73884.1; -.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 952 MW; EBC735B1E1F1B6D6 CRC64;

Query Match 44.0%; Score 11; DB 4; Length 8;
 Best Local Similarity 20.0%; Pred. No. 1e+06;
 Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
 :|:
 Db 1 MOTH 5

RESULT 13

Q9UMC7 PRELIMINARY; PRT; 8 AA.
 AC Q9UMC7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE SHMT protein (Fragment).
 GN SHMT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RA Chave K.J., Snell K., Sanders P.G.;
 RT "Isolation and characterization of human genomic sequences encoding
 RT cytosolic serine hydroxymethyltransferase.";
 RL Biochem. Soc. Trans. 25:53-53(1997).
 DR EMBL; Y14492; CAB54844.1; -.

FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 868 MW; 7C205721E44AB5B8 CRC64;

Query Match 44.0%; Score 11; DB 4; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHX 8
 :|:
 Db 4 NHL 6

RESULT 14
 Q9XSY1 PRELIMINARY; PRT; 8 AA.
 ID Q9XSY1;
 AC Q9XSY1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE Retinoblastoma protein (Fragment).
 GN RBL.

OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;

RP SEQUENCE FROM N.A.
 RX MEDLINE=97049323; PubMed=8994053;
 RA Venta P.J., Brouillette J.A., Yuzbasliyan-Gurkan V., Brewer G.J.;
 RT "Gene-specific universal mammalian sequence-tagged sites: application
 RT to the canine genome.";
 RL Biochem. Genet. 34:321-341(1996).

RP SEQUENCE FROM N.A.
 RA Venta P.J., Cao Y., Alexander L., Yuzbasliyan-Gurkan V.;
 RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (RBL)
 RT gene.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF155737; AAD38807.1; -.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 895 MW; 1425BBI86721E3 CRC64;

Query Match 44.0%; Score 11; DB 6; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH1 8
 DB 1 KHL 3

RESULT 15

Q8MGC9 PRELIMINARY; PRT; 8 AA.
 AC Q8MGC9;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE MADH dehydrogenase subunit 1 (Fragment).
 OS Upogebia affinis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Thalassinidea;
 OC Callinassoidae; Upogebidae; Upogebia.
 NC NCBI_TaxID=177247;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
 RA Cunningham C.W.;
 RT "Mitochondrial gene rearrangements support a hypothesis of parallel
 evolution to the crab-like form."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF36047; AAL31621.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KM Mitochondrion.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 978 MW; FE20573B5452C056 CRC64;

Query Match 44.0%; Score 11; DB 8; Length 8;
 Best Local Similarity 16.7%; Pred. No. 1e+06;
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH1 8
 DB 1 MIVVYL 6

RESULT 16

Q8L802 PRELIMINARY; PRT; 8 AA.
 AC Q8L802;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Pat (Fragment).
 GN PAT.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 NC NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ranning S.B., Berdal K.G., Vaitilingom M.M., Holst-Jensen A.;
 RT "Transformation event-specific quantitative real-time PCR for
 RT genetically modified Btl maize (Zea mays) and estimation of the
 RT impact of exogenous DNA on the limit of quantification."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY123624; AAM89275.1; -.
 FT NON TER 1

SQ SEQUENCE 8 AA; 909 MW; 6046C1B2D77412D7 CRC64;

Query Match 44.0%; Score 11; DB 10; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH1 8
 DB 3 RPTQI 8

RESULT 17

P79940 PRELIMINARY; PRT; 8 AA.
 AC P79940;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Xmei1-4 protein (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97202105; PubMed=9049632;
 RA Steelman S., Moskow J.J., Muzynski K., North C., Druck T.,
 RA Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.;
 RT "Identification of a conserved family of Meis1-related homeobox
 RT genes."
 RL Genome Res. 7:142-156(1997).
 DR EMBL; U68389; AAB19199.1; -.
 DR TRANSFAC; T03410; -.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 1187 MW; 278B51F37B11F40B CRC64;

Query Match 44.0%; Score 11; DB 13; Length 8;
 Best Local Similarity 16.7%; Pred. No. 1e+06;
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 QXVXH1 7
 DB 1 ERHBMH 6

RESULT 18

Q45615 PRELIMINARY; PRT; 8 AA.
 AC Q45615;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE GUTB protein (Fragment).
 GN GUTB.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=94253000; PubMed=8195086;
 RA Ye R., Wong S.L.;
 RT "Transcriptional regulation of the Bacillus subtilis glucitol
 RT dehydrogenase gene."
 RL J. Bacteriol. 176:3314-3320(1994).
 DR EMBL; L16626; AAA20875.1; -.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXXH 7
: : |
Db 1 MTH 3

RESULT 19

ID 09S443 PRELIMINARY; PRT; 8 AA.
AC 09S443;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
DE Beta-lactamase (Fragment).
GN PSE2.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R545;
RA Roy D., Coulombe M., Perron K., Roy P.H.;
RT "Characterization of a novel 6'-N-aminoglycoside acetyltransferase
RT gene aac(6')-IIC from the integron of a Chinese Pseudomonas aeruginosa
RT clinical isolate."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162771; AAD46628.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 930 MW; EBD5DDDD9D1A336 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;
Best Local Similarity 0.0%; Pred. No. 1e+06;
Matches 0; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 XXXVXHI 8
: : : : |
Db 1 MKTFPAIV 8

RESULT 20

ID 08G940 PRELIMINARY; PRT; 8 AA.
AC 08G940;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Plasmid group cp32-9, and Plasmid group cp32-12.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DN127C19-2, and Sh-2-82;
RC PLASMID=group cp32-9, and group cp32-12;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT SubMITTED (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142104; AAN17853.1; -.
DR EMBL; AY142097; AAN17907.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KM Plasmid.
FT NON TER 1
SQ SEQUENCE 8 AA; 1042 MW; 1437244330504373 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;
Best Local Similarity 0.0%; Pred. No. 1e+06;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHI 8

Db 1 KWIINKL 7
: : : : : |
Db 1 KWIINKL 7

RESULT 21

ID 005403 PRELIMINARY; PRT; 8 AA.
AC 005403;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)
DE DNA for ORF.s from chromosome XV (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=96021609; PubMed=8533473;
RA Zumslein E., Pearson B.M., Kalogetopoulos A., Schweizer M.;
RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames."
RL Yeast 11:975-986(1995).
DR EMBL; X83121; CAA58183.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 40.0%; Score 10; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXHI 8
: : : : |
Db 3 HNVVXI 8

RESULT 22

ID 013591 PRELIMINARY; PRT; 8 AA.
AC 013591;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)
DE ORF YNL337W (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermaler B., Piravandi E., Rinke M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC MIPS;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z71612; CAA96271.2; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 1005 MW; 5CA441E449C9C720 CRC64;

Query Match 40.0%; Score 10; DB 3; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXHI 7
: : : : |
Db 2 LFFNH 6

RESULT 23

Q98YTS PRELIMINARY; PRT; 8 AA.
ID Q98YTS

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AC O9BY5;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE cAMP responsive element moderator (Fragment).
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=11082082; PubMed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003677; F:DNA binding; NAS.
DR GO; GO:0006555; P:regulation of transcription, DNA-dependent; NAS.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 4; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
DB 1 DLYCH 5

RESULT 24
Q9UDZ4 PRELIMINARY; PRT; 8 AA.
ID Q9UDZ4;
AC Q9UDZ4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE RHD protein (Fragment).
GN RHD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97260406; PubMed=9106526;
RA Matsuishi G., Cherif-Zahar B., Mouru I., Carttron J.P.;
RT "Characterization of the recombination hot spot involved in the
RT genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
RT phenotype.";
RL Am. J. Hum. Genet. 60:808-817(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9306356; PubMed=1438298;
RA Le Van Kim C., Mouru I., Cherif-Zahar B., Raynal V., Cherrier C.,
RT "Molecular cloning and primary structure of the human blood group Rh
RT polypeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929(1992).
DR EMBL; Z97031; CAB09727.1; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1042 MW; D296944691FB5AB1 CRC64;

Query Match 40.0%; Score 10; DB 4; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 6 XHI 8
DB 3 YHM 5

RESULT 25
Q15893 PRELIMINARY; PRT; 8 AA.
ID Q15893;
AC Q15893;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE (Clone XP587A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32073; AAA73883.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;

Query Match 40.0%; Score 10; DB 4; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXVXH 6
DB 1 SQNPLQ 6

RESULT 26
Q9UMH9 PRELIMINARY; PRT; 8 AA.
ID Q9UMH9;
AC Q9UMH9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE RHCE protein (Fragment).
GN RHCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RA MEDLINE=97260406; PubMed=9106526;
RA Matsuishi G., Cherif-Zahar B., Mouru I., Carttron J.P.;
RT "Characterization of the recombination hot spot involved in the
RT genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
RT phenotype.";
RL Am. J. Hum. Genet. 60:808-817(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90349591; PubMed=1696722;
RA Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P.,
RA Hermand P., Salmon C., Carttron J.-P., Colin Y.;
RT "Molecular cloning and protein structure of a human blood group Rh
RT polypeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6243-6247(1990).
DR EMBL; Z97030; CAB09726.1; -.

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FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1049 MW; C007244691FB5AB1 CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 4; Length 8;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHI 8
DB 3 YHM 5

RESULT 27

Q81V87 PRELIMINARY; PRT; 8 AA.
AC Q81V87;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-JUN-2003 (TREMBlrel. 23, last sequence update)
DE D0107712.2 (Serine palmitoyltransferase, long chain subunit 2-like (Aminotransferase 2), variant 1) (Fragment).
GN SPTLC2L.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050320; CAD54807.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
KM Transferase.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 908 MW; 8E533682CEBB042 CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 4; Length 8;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXYXHI 8
DB 3 CCVWKI 8

RESULT 28

Q8MUN6 PRELIMINARY; PRT; 8 AA.
AC Q8MUN6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, last annotation update)
GN MPI.
OS Heliconius melipomene melipomene.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OX Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.
RN NCBI_TaxID=171917;
RP SEQUENCE FROM N.A.
RA STRAIN=STRI-B-441-Mpi-2;
RA Bull V., Beltman M., Bermingham E., Jiggins C., McMillan O., Mallet J.;
RT "Molecular evidence for gene flow between species of Heliconius";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516247; AAM61933.1; -.
DR GO; GO:0016853; F:isomerase activity; IEA.
KM Isomerase.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 977 MW; 16E736DB1D1EAA3 CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 5; Length 8;
Matches 1; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 XQXXVXH 7
DB 2 DHAEQLH 8

RESULT 29

Q86BS9 PRELIMINARY; PRT; 8 AA.
AC Q86BS9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)
DE Cyclin B (Fragment).
GN CYCLIN B.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OX Strongylocentrotus.
RN NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96027756; PubMed=7546293;
RA Thatcher J.D., McBride B., Katula K.S.;
RT "Promoter binding factors regulating cyclin B transcription in the sea urchin embryo";
RL DNA Cell Biol. 14:869-881(1995).
DR EMBL; S80441; AAP32224.1; -.
KM Cyclin.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 897 MW; EE645411ADD1EDD6 CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 5; Length 8;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXH 7
DB 1 MAH 3

RESULT 30

Q9TT78 PRELIMINARY; PRT; 8 AA.
AC Q9TT78;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)
GN TS.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015404; PubMed=1130975;
RA Brouillette J.A., Andrew J.R., Venta P.J.;
RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence method";
RL Mamm. Genome 11:1079-1086(2000).
DR EMBL; AF202073; AAF20918.1; -.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 899 MW; 6731A1B059CA867 CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
DB 2 GDFH 6

RESULT 31

O9BF82 PRELIMINARY; PRT; 8 AA.
AC O9BF82; (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
GN CAMP responsive element moderator (Fragment).
OS Urus arctos (Brown bear) (Grizzly bear).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=9644;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals."
RL Nature 409:614-618(2001).
DR EMBL: AY011683; AAC47591.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
DB 1 DLVCH 5

RESULT 32

O9BFC2 PRELIMINARY; PRT; 8 AA.
AC O9BFC2; (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
GN CAMP responsive element moderator (Fragment).
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals."
RL Nature 409:614-618(2001).
DR EMBL: AY011621; AAC47536.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
DB 1 DLVCH 5

RESULT 33

O9BF90 PRELIMINARY; PRT; 8 AA.
AC O9BF90; (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
GN CAMP responsive element moderator (Fragment).
OS Tragelaphus eurycerus (Bongo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Tragelaphus.
OX NCBI_TaxID=69297;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals."
RL Nature 409:614-618(2001).
DR EMBL: AY011673; AAC47583.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
DB 1 DLVCH 5

RESULT 34

O9BFB1 PRELIMINARY; PRT; 8 AA.
AC O9BFB1; (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
GN CAMP responsive element moderator (Fragment).
OS Echinos telfairi (Leeser hedgehog tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecidae; Echinos.
OX NCBI_TaxID=9371;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals."
RL Nature 409:614-618(2001).
DR EMBL: AY011632; AAC47547.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
DB 1 DLVCH 5

RESULT 35

O9BFA1 PRELIMINARY; PRT; 8 AA.
AC O9BFA1; (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

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DE  CAMP responsive element moderator (Fragment).
GN  CREM.
OS  Ateles fusciceps (Brown-headed spider monkey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
OX  NCBI_TaxID=9508;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21082082; PubMed=11214319;
RA  Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA  O'Brien S.J.;
RT  "Molecular phylogenetics and the origins of placental mammals.";
RL  Nature 409:614-618(2001).
DR  EMBL; AY011660; AAC47571.1; -.
FT  NON TER 1
SQ  SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 36
Q9BFB7 PRELIMINARY; PRT; 8 AA.
ID Q9BFB7;
AC Q9BFB7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Tapirus indicus (Asiatic tapir) (Malayan tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=9802;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011678; AAC47586.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 37
Q9BFB9 PRELIMINARY; PRT; 8 AA.
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AC Q9BFB9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Euphractus.
OX NCBI_TaxID=143300;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011624; AAC47539.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 38
Q9BFB8 PRELIMINARY; PRT; 8 AA.
ID Q9BFB8;
AC Q9BFB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Chaetophractus villosus (South American armadillo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophractus.
OX NCBI_TaxID=29080;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011625; AAC47540.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 39
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ID Q9BFA0;
AC Q9BFA0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).

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DR EMBL; AY011661; AAC47572.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C31EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
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Db 1 DLVCH 5

RESULT 40
O9BFA8 PRELIMINARY; PRT; 8 AA.
AC O9BFA8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Loxodonta africana (African elephant).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Loxodonta.
OX NCBI_TaxID=9785;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011635; AAC47550.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
   ::|
Db 1 DLVCH 5

RESULT 41
O9BFA9 PRELIMINARY; PRT; 8 AA.
ID O9BFA9;
AC O9BFA9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Procyon capensis (Cape hyrax) (Rock dassie).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Hyracoidea; Procaviidae; Procavia.
OX NCBI_TaxID=9813;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011634; AAC47549.1; -.
FT NON TER 1
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Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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OY 3 XXVXH 7
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Db 1 DLVCH 5

RESULT 42
O9BFB2 PRELIMINARY; PRT; 8 AA.
ID O9BFB2;
AC O9BFB2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Sorex araneus (Eurasian common shrew) (European shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
OX NCBI_TaxID=42254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011631; AAC47546.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
   ::|
Db 1 DLVCH 5

RESULT 43
O9BFB5 PRELIMINARY; PRT; 8 AA.
ID O9BFB5;
AC O9BFB5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Erinaceus concolor (Eastern European hedgehog) (Erinaceus roumanicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=37316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011628; AAC47543.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
   ::|
Db 1 DLVCH 5

RESULT 44

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Q9BFB6
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AC Q9BFB6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Myrmecophaga tridactyla (Giant anteater).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Myrmecophagidae; Myrmecophaga.
OX NCBI_TaxID=71006;
RN [1]
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RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011627; AAG47542.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 45
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ID Q9BFB3 PRELIMINARY; PRT; 8 AA.
AC Q9BFB3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Condylura cristata (Star-nosed mole).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Talpidae; Condylura.
OX NCBI_TaxID=143302;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011630; AAG47545.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

Search completed: August 19, 2004, 15:50:49
Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 ; Search time 13.5 Seconds

(without alignments)
30.593 Million cell updates/secTitle: VARIANT1
Perfect score: 25
Sequence: 1 XQXXVHL 8Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 13858

Minimum DB seq length: 8
Maximum DB seq length: 8Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/prodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	25	100.0	8 1 US-08-168-390-11	Sequence 11, App1
2	25	100.0	8 1 US-08-168-390-12	Sequence 12, App1
3	25	100.0	8 2 US-08-337-127-9	Sequence 9, App1
4	25	100.0	8 4 US-09-260-846-9	Sequence 9, App1
5	25	100.0	8 4 US-09-248-381-16	Sequence 16, App1
6	25	100.0	8 4 US-09-248-381-17	Sequence 17, App1
7	25	100.0	8 6 5217955-32	Patent No. 5217955
8	25	100.0	8 6 5217955-34	Patent No. 5217955
9	25	100.0	8 6 5217955-35	Patent No. 5217955
10	25	100.0	8 6 5217955-36	Patent No. 5217955
11	23	92.0	8 4 US-09-248-381-18	Sequence 18, App1
12	23	92.0	8 4 US-09-248-381-19	Sequence 19, App1
13	23	88.0	8 6 5217955-37	Patent No. 5217955
14	21	84.0	8 1 US-08-031-325A-27	Sequence 27, App1
15	21	84.0	8 2 US-08-337-127-4	Sequence 4, App1
16	21	84.0	8 2 US-08-337-127-8	Sequence 8, App1
17	21	84.0	8 4 US-09-260-846-4	Sequence 4, App1
18	21	84.0	8 4 US-09-260-846-8	Sequence 8, App1
19	21	84.0	8 4 US-09-248-381-6	Sequence 6, App1
20	21	84.0	8 6 5217955-31	Patent No. 5217955
21	21	84.0	8 6 5217955-33	Patent No. 5217955
22	21	84.0	8 6 5217955-38	Patent No. 5217955
23	20	80.0	8 1 US-08-168-390-13	Sequence 13, App1
24	20	80.0	8 1 US-08-168-390-14	Sequence 14, App1
25	19	76.0	8 1 US-08-387-634-3	Sequence 3, App1
26	19	76.0	8 4 US-09-515-965A-1846	Sequence 1846, App1
27	19	76.0	8 6 5217955-25	Patent No. 5217955

28	19	76.0	8 6 5217955-27	Patent No. 5217955
29	19	76.0	8 6 5217955-28	Patent No. 5217955
30	18	72.0	8 3 US-08-444-818-632	Sequence 632, App1
31	18	72.0	8 3 US-09-011-961-16	Sequence 16, App1
32	18	72.0	8 4 US-09-428-082B-537	Sequence 537, App1
33	18	72.0	8 4 US-09-428-082B-539	Sequence 539, App1
34	17	68.0	8 1 US-08-427-993B-4	Sequence 4, App1
35	17	68.0	8 2 US-08-478-609A-4	Sequence 4, App1
36	17	68.0	8 3 US-08-816-346-20	Sequence 20, App1
37	17	68.0	8 3 US-08-444-818-375	Sequence 375, App1
38	17	68.0	8 3 US-08-444-818-633	Sequence 633, App1
39	17	68.0	8 4 US-09-335-411-20	Sequence 20, App1
40	17	68.0	8 3 US-09-515-965A-1889	Sequence 1889, App1
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42	16	64.0	8 1 US-08-297-494-34	Sequence 34, App1
43	16	64.0	8 1 US-08-297-510-34	Sequence 34, App1
44	16	64.0	8 1 US-08-479-532-34	Sequence 34, App1
45	16	64.0	8 1 US-08-571-985-22	Sequence 22, App1

ALIGNMENTS

RESULT 1
US-08-168-390-11
Sequence 11, Application US/08168390
Patent No. 5620955
GENERAL INFORMATION:
APPLICANT: Knight, Martha
APPLICANT: Takahashi, Kazuyuki
APPLICANT: Chandrasekhar, Bhaskar
TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,390
CLASSIFICATION: 530
FILING DATE: Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0871.0040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "The amino-terminal residue
comprises one of several chemical end caps."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /note= "The carboxy-terminal
residue comprises an ethyl ester."
US-08-168-390-11

Query Match 100.0%; Score 25; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 X0XXVXHL 8
DB 1 N0MAVGH 8

RESULT 2
US-08-168-390-12
; Sequence 12, Application US/08168390
; Patent No. 5620955
; GENERAL INFORMATION:
; APPLICANT: Knight, Martha
; APPLICANT: Takahashi, Kazuyuki
; APPLICANT: Chandrasekhar, Bhaskar
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/168,390
; FILING DATE: Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0871.0040001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; TELEX: 248636 SKK
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "The amino-terminal residue
; OTHER INFORMATION: comprises one of several chemical end caps."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "The alanine at position 6
; OTHER INFORMATION: is dextrorotatory alanine."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "The carboxy-terminal
; OTHER INFORMATION: residue comprises an ethyl ester."
; US-08-168-390-12

Query Match 100.0%; Score 25; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 X0XXVXHL 8
DB 1 N0MAVGH 8

RESULT 3
US-08-337-127-9
; Sequence 9, Application US/08337127
; Patent No. 5877277
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun H.
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 50z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,127
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/779,039
; FILING DATE: 10/18/91
; APPLICATION NUMBER: 07/502,438
; FILING DATE: 03/30/90
; APPLICATION NUMBER: 07/397,169
; FILING DATE: 08/21/89
; APPLICATION NUMBER: 07/376,555
; FILING DATE: 07/07/89
; APPLICATION NUMBER: 07/317,941
; FILING DATE: 03/02/89
; APPLICATION NUMBER: 07/282,328
; FILING DATE: 12/09/88
; APPLICATION NUMBER: 07/257,998
; FILING DATE: 10/14/88
; APPLICATION NUMBER: 07/248,771
; FILING DATE: 09/23/88
; APPLICATION NUMBER: 07/207,759
; FILING DATE: 06/16/88
; APPLICATION NUMBER: 07/204,171
; FILING DATE: 06/08/88
; APPLICATION NUMBER: 07/173,311
; FILING DATE: 03/25/88
; APPLICATION NUMBER: 07/100,571
; FILING DATE: 09/24/87
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/00900D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence contains at
; OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,
; OTHER INFORMATION: and has an methyl ester C-terminus (i.e., COOCH3),
; OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COOH).

US-09-337-127-9

Query Match 100.0%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 4; Mismatches 0;

Qy 1 XQXXVXHL 8
|:|:|:|
Db 1 EQWAVGHL 8

RESULT 4
US-09-260-846-9
Sequence 9, Application US/09260846
Patent No. 6307017
GENERAL INFORMATION:
APPLICANT: COY, David H.
APPLICANT: Moreau, Jacques-Pierre
APPLICANT: Kim, Sun Hyuk
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
FILE REFERENCE: 00537/009003
CURRENT APPLICATION NUMBER: US/09/260,846
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: pyroglutamate
FEATURE:
OTHER INFORMATION: this peptide has a methyllester c-terminus
US-09-260-846-9

Query Match 100.0%; Score 25; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 4; Mismatches 0;

Qy 1 XQXXVXHL 8
|:|:|:|
Db 1 EQWAVGHL 8

RESULT 5
US-09-248-381-16
Sequence 16, Application US/09248381
Patent No. 6492330
GENERAL INFORMATION:
APPLICANT: MUKHERJEE, RAMA
APPLICANT: JAGGI, MANU
APPLICANT: PRASAD, SUDHANAND
APPLICANT: BURMAN, ANAND C
APPLICANT: RAJENDRAN, PRAVEEN
APPLICANT: NATHUR, ARCHANA
APPLICANT: SINGH, ANU T
TITLE OF INVENTION: ANTITANGIOGENIC DRUGS
FILE REFERENCE: U 011695-8
CURRENT APPLICATION NUMBER: US/09/248,381
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: This peptide
OTHER INFORMATION: was synthetically generated.

FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe;
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)
OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb
US-09-248-381-16

Query Match 100.0%; Score 25; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0;

Qy 1 XQXXVXHL 8
|:|:|:|
Db 1 XQWVXHL 8

RESULT 6
US-09-248-381-17
Sequence 17, Application US/09248381
Patent No. 6492330
GENERAL INFORMATION:
APPLICANT: MUKHERJEE, RAMA
APPLICANT: JAGGI, MANU
APPLICANT: PRASAD, SUDHANAND
APPLICANT: BURMAN, ANAND C
APPLICANT: RAJENDRAN, PRAVEEN
APPLICANT: NATHUR, ARCHANA
APPLICANT: SINGH, ANU T
TITLE OF INVENTION: ANTITANGIOGENIC DRUGS
FILE REFERENCE: U 011695-8
CURRENT APPLICATION NUMBER: US/09/248,381
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: This peptide
OTHER INFORMATION: was synthetically generated.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)
OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb
US-09-248-381-17

Query Match 100.0%; Score 25; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0;

Qy 1 XQXXVXHL 8
|:|:|:|
Db 1 XQWVXHL 8

RESULT 7
5217955-32
Patent No. 5217955
APPLICANT: ABOGDE, ARTHUR E.; MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:32:
; LENGTH: 8
5217955-32
```

```
Query Match 100.0%; Score 25; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XXXXXVHL 8
   ||::||
Db 1 FQWAVVGH 8
```

```
RESULT 8
5217955-34
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:34:
; LENGTH: 8
5217955-34
```

```
Query Match 100.0%; Score 25; DB 6; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XXXXXVHL 8
   ||::||
Db 1 XQWAVVGH 8
```

```
RESULT 9
5217955-35
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:35:
; LENGTH: 8
5217955-35
```

```
Query Match 100.0%; Score 25; DB 6; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XXXXXVHL 8
   ||::||
Db 1 XQWAVVGH 8
```

```
RESULT 10
5217955-36
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:36:
; LENGTH: 8
5217955-36
```

```
Query Match 100.0%; Score 25; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 XXXXXVHL 8
   ||::||
Db 1 FQWAVVGH 8
```

```
RESULT 11
US-09-248-381-18
; Sequence 18, Application US/09248381
; Patent No. 6492330
; GENERAL INFORMATION:
; APPLICANT: MUKHERJEE, RAMA
; APPLICANT: JAGGI, MANU
; APPLICANT: PRASAD, SUDHANAND
; APPLICANT: BURMAN, ANAND C
; APPLICANT: RAJENDRAN, PRAVEEN
; APPLICANT: MATUR, ARCHANA
; APPLICANT: SINGH, ANU T
; TITLE OF INVENTION: ANTITUMORIC DRUGS
; FILE REFERENCE: U 011695-8
; CURRENT APPLICATION NUMBER: US/09/248,381
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This peptide
; OTHER INFORMATION: was synthetically generated.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
; NAME/KEY: MOD_RES
; LOCATION: (4)-
; OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Aib
; US-09-248-381-18
```

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Query Match 92.0%; Score 23; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 XXXXXVHL 8
   ||::||
Db 1 XQWAVVGH 8
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RESULT 12
US-09-248-381-19
; Sequence 19, Application US/09248381
; Patent No. 6492330
; GENERAL INFORMATION:
; APPLICANT: MUKHERJEE, RAMA
; APPLICANT: JAGGI, MANU
; APPLICANT: PRASAD, SUDHANAND
; APPLICANT: BURMAN, ANAND C
; APPLICANT: RAJENDRAN, PRAVEEN
; APPLICANT: MATHUR, ARCHANA
; APPLICANT: SINGH, ANU T
; TITLE OF INVENTION: ANTIANGIOGENIC DRUGS
; FILE REFERENCE: U 011695-8
; CURRENT APPLICATION NUMBER: US/09/248,381
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This peptide
; OTHER INFORMATION: was synthetically generated.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb
US-09-248-381-19

Query Match 92.0%; Score 23; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8
Db 1 XQWAVXHI 8

RESULT 13
5217955-37
; Patent No. 5217955
; APPLICANT: ABOGDE, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO: 37
; LENGTH: 8
5217955-37

Query Match 88.0%; Score 22; DB 6; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8
Db 1 FEWAVXHL 8

RESULT 14

US-08-031-325A-27
; Sequence 27, Application US/08031325A
; Patent No. 5369094
; GENERAL INFORMATION:
; APPLICANT: Schally, Andrew V.
; APPLICANT: Cai, Renzhi
; TITLE OF INVENTION: POLYPEPTIDE BOMBESIN ANTAGONISTS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OMRI M. BEHR, ESQ
; STREET: 325 PIERSON AVENUE
; CITY: EDISON
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 08837
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/031,325A
; FILING DATE: 15-MAR-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/619,747
; FILING DATE: 29-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BEHR, OMRI M.
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHAL3.0-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 494-5240
; TELEFAX: (908) 494-0428
; TELEX: 511642 BEPATEDIN
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Res 1 = (R1) (R2)-A0-A1, where A0
; OTHER INFORMATION: = deleted; A1 = D-Phe, D-Tyr or D-Nal; R1 and R2 = H"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 8
; OTHER INFORMATION: /note= "Res 8 = A8-W, where W = -N(R8)-
; OTHER INFORMATION: CH(Z1)-R4-CH(Z2)-CO-V, where R4 = CH2NH; Z1 = -CH2CH(CH3)2; Z2
; OTHER INFORMATION: H or
; OTHER INFORMATION: COB1, where E1 = C1-20 alkyl"
US-08-031-325A-27

Query Match 84.0%; Score 21; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 7
Db 1 XQWAVXHI 7

RESULT 15
US-08-337-127-4
; Sequence 4, Application US/08337127
; Patent No. 5877277
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre

APPLICANT: Kim, Sun H.
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
TITLE OF INVENTION: ANALOGS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,127
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/779,039
FILING DATE: 10/18/91
APPLICATION NUMBER: 07/502,438
FILING DATE: 03/30/90
APPLICATION NUMBER: 07/397,169
FILING DATE: 08/21/89
APPLICATION NUMBER: 07/376,555
FILING DATE: 07/07/89
APPLICATION NUMBER: 07/317,941
FILING DATE: 03/02/89
APPLICATION NUMBER: 07/282,328
FILING DATE: 12/09/88
APPLICATION NUMBER: 07/257,998
FILING DATE: 10/14/88
APPLICATION NUMBER: 07/248,771
FILING DATE: 09/23/88
APPLICATION NUMBER: 07/207,759
FILING DATE: 06/16/88
APPLICATION NUMBER: 07/204,171
FILING DATE: 06/08/88
APPLICATION NUMBER: 07/173,311
FILING DATE: 03/25/88
APPLICATION NUMBER: 07/100,571
FILING DATE: 09/24/87
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00537/00900D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The sequence contains at
OTHER INFORMATION: position 1 a pyroglutamate,
OTHER INFORMATION: and has an amide C-terminus (i.e., COYNH2), rather
OTHER INFORMATION: than
OTHER INFORMATION: a carboxyl C-terminus (i.e., COYOH). Xaa stands for
OTHER INFORMATION: statine.
US-08-337-127-4

Query Match 84.0%; Score 21; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

1 XQXXVXH 7

Db :|:|:|
1 EQWAVGH 7
RESULT 16
US-08-337-127-8
Sequence 8, Application US/08337127
Patent No. 5877277
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Moreau, Jacques-Pierre
APPLICANT: Kim, Sun H.
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
TITLE OF INVENTION: ANALOGS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,127
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/779,039
FILING DATE: 10/18/91
APPLICATION NUMBER: 07/502,438
FILING DATE: 03/30/90
APPLICATION NUMBER: 07/397,169
FILING DATE: 08/21/89
APPLICATION NUMBER: 07/376,555
FILING DATE: 07/07/89
APPLICATION NUMBER: 07/317,941
FILING DATE: 03/02/89
APPLICATION NUMBER: 07/282,328
FILING DATE: 12/09/88
APPLICATION NUMBER: 07/257,998
FILING DATE: 10/14/88
APPLICATION NUMBER: 07/248,771
FILING DATE: 09/23/88
APPLICATION NUMBER: 07/207,759
FILING DATE: 06/16/88
APPLICATION NUMBER: 07/204,171
FILING DATE: 06/08/88
APPLICATION NUMBER: 07/173,311
FILING DATE: 03/25/88
APPLICATION NUMBER: 07/100,571
FILING DATE: 09/24/87
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00537/00900D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The sequence contains at
OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,

OTHER INFORMATION: and has an methyl ester C-terminus (i.e., COYCH₃),
OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COYOH).
US-08-337-127-8

Query Match 84.0%; Score 21; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 7
DB 1 EQWAVGH 7

RESULT 17
US-09-260-846-4
Sequence 4, Application US/09260846
Patent No. 6307017
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Moreau, Jacques-Pierre
APPLICANT: Kim, Sun Hyuk
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
FILE REFERENCE: 00537/009000
CURRENT APPLICATION NUMBER: US/09/260,846
CURRENT FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide

NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: pyroglutamate
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: statine
FEATURE:
OTHER INFORMATION: this peptide has an amidated c-terminus
US-09-260-846-4

Query Match 84.0%; Score 21; DB 4; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 7
DB 1 EQWAVGH 7

RESULT 18
US-09-260-846-8
Sequence 8, Application US/09260846
Patent No. 6307017
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Moreau, Jacques-Pierre
APPLICANT: Kim, Sun Hyuk
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
FILE REFERENCE: 00537/009000
CURRENT APPLICATION NUMBER: US/09/260,846
CURRENT FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

US-09-260-846-8
Sequence 8, Application US/09260846
Patent No. 6307017
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Moreau, Jacques-Pierre
APPLICANT: Kim, Sun Hyuk
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
FILE REFERENCE: 00537/009000
CURRENT APPLICATION NUMBER: US/09/260,846
CURRENT FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: pyroglutamate
FEATURE:
OTHER INFORMATION: this peptide has a methyl ester c-terminus
US-09-260-846-8

Query Match 84.0%; Score 21; DB 4; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 7
DB 1 EQWAVGH 7

RESULT 19
US-09-248-381-6
Sequence 6, Application US/09248381
Patent No. 6492330
GENERAL INFORMATION:
APPLICANT: MURHERJEE, RAMA
APPLICANT: JAGGI, MANU
APPLICANT: PRASAD, SUDHANAND
APPLICANT: BURMAN, ANAND C
APPLICANT: RAJENDRAN, PRAVEEN
APPLICANT: MATHER, ARCHANA
APPLICANT: SINGH, ANU T
TITLE OF INVENTION: ANTIANGIOGENIC DRUGS
FILE REFERENCE: U 011695-8
CURRENT APPLICATION NUMBER: US/09/248,381
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: This peptide
OTHER INFORMATION: was synthetically generated.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: /product=leucine N-ethylamide/label=Leu-NHET
US-09-248-381-6

Query Match 84.0%; Score 21; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 7
DB 1 EQWAVGH 7

RESULT 20
5217955-31
Patent No. 5217955
APPLICANT: ABOGDE, ARTHUR B.; MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUBROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO:31:
LENGTH: 8
5217955-31

Query Match 84.0%; Score 21; DB 6; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXH 7
|:|:|:
DB 1 XOMAVGH 7

RESULT 21
5217955-33
Patent No. 5217955
APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO:33:
LENGTH: 8
5217955-33

Query Match 84.0%; Score 21; DB 6; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXH 7
|:|:|:
DB 1 EOMAVGH 7

RESULT 22
5217955-38
Patent No. 5217955
APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO:38:
LENGTH: 8
5217955-38

Query Match 84.0%; Score 21; DB 6; Length 9;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXH 7
|:|:|:
DB 1 EOMAVGH 7

RESULT 23
US-08-168-390-13
Sequence 13, Application US/08168390
Patent No. 5620955
GENERAL INFORMATION:
APPLICANT: Knight, Martha
APPLICANT: Takahashi, Kazayuki
APPLICANT: Chandrasekhar, Bhaskar
TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,390
FILING DATE: Herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0871.0040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
TELEX: 248636 SSK

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear

FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "The amino-terminal residue
comprises one of several chemical end caps."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /note= "The carboxy-terminal
residue comprises an ethyl ester."
US-08-168-390-13

Query Match 80.0%; Score 20; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XXXXXH 8
|:|:|:
DB 1 NHMAVGH 8

RESULT 24
US-08-168-390-14
Sequence 14, Application US/08168390
Patent No. 5620955
GENERAL INFORMATION:
APPLICANT: Knight, Martha
APPLICANT: Takahashi, Kazayuki
APPLICANT: Chandrasekhar, Bhaskar
TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,390
FILING DATE: Herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0871.0040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "The amino-terminal residue
FEATURE:
OTHER INFORMATION: comprises one of several chemical end caps."
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note= "The alanine at position 6
FEATURE:
OTHER INFORMATION: is dextrorotatory alanine."
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /note= "The carboxy-terminal
OTHER INFORMATION: residue comprises an ethyl ester."
US-08-168-390-14
Query Match 80.0%; Score 20; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 3; Conservative 4; Mismatches 1;
QY 1 XQXVXHL 8
DB 1 NHVAVHL 8
RESULT 25
US-08-387-634-3
Sequence 3, Application US/08387634
Patent No. 5767235
GENERAL INFORMATION:
APPLICANT: Kim, Sun Hyuk
APPLICANT: Moreau, Jacques-Pierre
TITLE OF INVENTION: LINEAR THERAPEUTIC PEPTIDES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,634
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/929,306A
FILING DATE: 08/13/92
APPLICATION NUMBER: US/07/520,226
FILING DATE: 05/09/90
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T. and Tsao, Y. Rocky
REGISTRATION NUMBER: 30,162 and 34,053
REFERENCE/DOCKET NUMBER: 00537/040002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
FEATURE:
OTHER INFORMATION:
OTHER INFORMATION: The sequence contains at position 1 an acetylated His, rather
OTHER INFORMATION: than a His, and has an amide C-terminus (i.e., COOH).
US-08-387-634-3
Query Match 76.0%; Score 19; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 XXVXHL 8
DB 2 WVGXHL 7
RESULT 26
US-09-515-965A-1846
Sequence 1846, Application US/09515965A
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
FILE REFERENCE: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1846
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1846
Query Match 76.0%; Score 19; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 XXVXHL 8
DB 4 WVGXHL 8

Db 3 SKVXHL 8

RESULT 27
5217955-25
; Patent No. 5217955
; APPLICANT: ABOUDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:25:
; LENGTH: 8
5217955-25

Query Match 76.0%; Score 19; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
:::|:|
Db 2 WAVXHL 7

RESULT 28
5217955-27
; Patent No. 5217955
; APPLICANT: ABOUDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:27:
; LENGTH: 8
5217955-27

Query Match 76.0%; Score 19; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
:::|:|
Db 2 WAVXHL 7

RESULT 29
5217955-28
; Patent No. 5217955
; APPLICANT: ABOUDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:28:
; LENGTH: 8
5217955-28

Query Match 76.0%; Score 19; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
:::|:|
Db 2 WAVXHL 7

; FILING DATE: 15-SEP-1989
; SEQ ID NO:28:
; LENGTH: 8
5217955-28

Query Match 76.0%; Score 19; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
:::|:|
Db 2 WAVXHL 7

RESULT 30
US-08-444-818-632
; Sequence 632, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 632:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-444-818-632

Query Match 72.0%; Score 18; DB 3; Length 8;
Best Local Similarity 28.6%; Pred. No. 3e+05;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHL 8
:::|:|
Db 1 RKAVTHI 7

RESULT 31
US-09-011-961-16
; Sequence 16, Application US/09011961
; Patent No. 6197536
; GENERAL INFORMATION:
; APPLICANT: STEINKUEHLER, Christian

APPLICANT: PESSI, Antonello
APPLICANT: BIANCHI, Elisabetta
APPLICANT: TALIANI, Marina
APPLICANT: TOMEI, Licia
APPLICANT: URBANI, Andrea
APPLICANT: DE FRANCESCO, Raffaele
APPLICANT: NARJES, Frank
TITLE OF INVENTION: METHODOLOGY TO PRODUCE, AND PURIFY AND
TITLE OF INVENTION: ASSAY POLYPEPTIDES WITH THE PROTEOLYTIC ACTIVITY OF THE
TITLE OF INVENTION: HCV NS3 PROTEASE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,961
FILING DATE: 23-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT96/00163
FILING DATE: 20-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM95A000573
FILING DATE: 22-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: STEINKUHLER=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /note= "Xaa is Ac-Met"
US-09-011-961-16

Query Match 72.0%; Score 18; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8
|:|:|
Db 1 XECCASHL 8

RESULT 32
US-09-428-082B-537
Sequence 537, Application US/09428082B
Patent No. 6660843
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527

CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.1
SEQ ID NO 537
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE
US-09-428-082B-537

Query Match 72.0%; Score 18; DB 4; Length 8;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 XVXHL 8
|:|:|
Db 1 KVFHL 5

RESULT 33
US-09-428-082B-539
Sequence 539, Application US/09428082B
Patent No. 6660843
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.1
SEQ ID NO 539
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE
US-09-428-082B-539

Query Match 72.0%; Score 18; DB 4; Length 8;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
|:|:|
Db 3 FHLHL 8

RESULT 34
US-08-427-993B-4
Sequence 4, Application US/08427993B
Patent No. 5668013
GENERAL INFORMATION:
APPLICANT: Posner, Jerome B.
APPLICANT: Furneaux, Henry M.
TITLE OF INVENTION: ANTIGEN RECOGNIZED BY PATIENTS WITH
TITLE OF INVENTION: ANTIBODY ASSOCIATED CEREBELLAR DEGENERATION,
TITLE OF INVENTION: DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,993B
FILING DATE: April 24, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38199-1/JPM/JKM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-427-993B-4

Query Match 68.0%; Score 17; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 3e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XOXVXHL 8
Db 1 LOTRIANL 8

RESULT 35
US-08-478-609A-4
Sequence 4, Application US/08478609A
Patent No. 5925526
GENERAL INFORMATION:
APPLICANT: Posner, Jerome B.
TITLE OF INVENTION: Furneaux, Henry M.
TITLE OF INVENTION: ANTIGEN RECOGNIZED BY PATIENTS WITH
TITLE OF INVENTION: ANTIBODY ASSOCIATED CEREBELLAR DEGENERATION,
TITLE OF INVENTION: DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,609A
FILING DATE: June 5, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38199-12/JPM/JKM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-478-609A-4

Query Match 68.0%; Score 17; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 3e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XOXVXHL 8
Db 1 LOTRIANL 8

RESULT 36
US-08-816-346-20
Sequence 20, Application US/08816346
Patent No. 6127325
GENERAL INFORMATION:
APPLICANT: Crystal, Ronald G.
APPLICANT: Falck-Pedersen, Erik
APPLICANT: Gall, Jason
APPLICANT: Kovacs, Imre
TITLE OF INVENTION: Wickham, Thomas J.
TITLE OF INVENTION: CHIMERIC ADENO VIRAL COAT PROTEIN AND
NUMBER OF SEQUENCES: 60
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA - 4900
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,346
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 67167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/616-5600
TELEFAX: 312/616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-816-346-20

Query Match 68.0%; Score 17; DB 3; Length 8;
Best Local Similarity 14.3%; Pred. No. 3e+05;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XOXVXHL 7
Db 1 YETRIANH 7

RESULT 37
US-08-444-818-375
Sequence 375, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisha A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 375:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-375

Query Match 68.0%; Score 17; DB 3; Length 8;
Best Local Similarity 25.0%; Pred. No. 3e+05;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 XOXVXHL 8
DB 1 LSTGLIHL 8

RESULT 38
US-08-444-818-633
Sequence 633, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisha A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 633:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-633

Query Match 68.0%; Score 17; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXYVXHL 8
DB 1 KAVTHI 6

RESULT 39
US-09-335-411-20
Sequence 20, Application US/09335411
Patent No. 6153435
GENERAL INFORMATION:
APPLICANT: Crystal, Ronald G.
APPLICANT: Faick-Pedersen, Erik
APPLICANT: Gall, Jason
APPLICANT: Kovacs, Imre
APPLICANT: Micham, Thomas J.
TITLE OF INVENTION: CHIMERIC ADENO VIRAL COAT PROTEIN AND
METHODS OF USING SAME
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA - 4900
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,411
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,346
FILING DATE:
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 67167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/616-5600
TELEFAX: 312/616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-335-411-20

Query Match 68.0%; Score 17; DB 3; Length 8;
Best Local Similarity 14.3%; Pred. No. 3e+05;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7
Db 1 YETELNH 7

RESULT 40
US-09-515-965A-1889
Sequence 1889, Application US/09515965A
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1889
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1889

Query Match 68.0%; Score 17; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXHL 8
Db 1 VLHL 4

RESULT 41
US-07-872-644-34
Sequence 34, Application US/07872644
Patent No. 5389527
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/872,644
FILING DATE: 19920420
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5389527and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-872-644-34

Query Match 64.0%; Score 16; DB 1; Length 8;
Best Local Similarity 14.3%; Pred. No. 3e+05;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHL 8
Db 1 EMMNYTHM 7

RESULT 42
US-08-297-494-34
Sequence 34, Application US/08297494
Patent No. 5580771
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,494
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5580771and, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-297-494-34

Query Match 64.0%; Score 16; DB 1; Length 8;
Best Local Similarity 14.3%; Pred. No. 3e+05;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXXVXHL 8
Db 1 EMMMYHM 7

RESULT 43
US-08-297-510-34
Sequence 34, Application US/08297510
Patent No. 5602019

GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonenbourg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,510
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5602019and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-297-510-34

Query Match 64.0%; Score 16; DB 1; Length 8;

Best Local Similarity 14.3%; Pred. No. 3e+05;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXXVXHL 8
Db 1 EMMMYHM 7

RESULT 44
US-08-479-532-34
Sequence 34, Application US/08479532
Patent No. 576752
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonenbourg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,532
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/297,494
FILING DATE:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 576752and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-479-532-34

Query Match 64.0%; Score 16; DB 1; Length 8;
Best Local Similarity 14.3%; Pred. No. 3e+05;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXXVXHL 8
Db 1 EMMMYHM 7

RESULT 45
US-08-571-985-22
Sequence 22, Application US/08571985
Patent No. 5783557
GENERAL INFORMATION:

APPLICANT: Birstein, Yigal
APPLICANT: Trainin, Nathan
APPLICANT: Rycus, Avigail
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical
TITLE OF INVENTION: Compositions Comprising Them
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 578357thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: USA
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,985
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106214
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2163.00048
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-571-985-22

Query Match 64.0%; Score 16; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 3e+05;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 XQXXVXHL 8
Db 1 LEDGPKHL 8

Search completed: August 19, 2004, 15:52:27
Job time : 14.5 secs

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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:51:28 ; Search time 38 Seconds
(without alignments)
66.159 Million cell updates/sec

Title: VARIANT1
Perfect score: 25
Sequence: 1 XQXVXHL 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 31425058 residues
Total number of hits satisfying chosen parameters: 16665

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	25	100.0	8 10 US-09-896-903C-2	Sequence 2, App11
2	25	100.0	8 14 US-10-186-226A-2	Sequence 2, App11
3	25	100.0	8 16 US-10-329-321A-2	Sequence 2, App11
4	24	96.0	8 9 US-09-766-347-1	Sequence 1, App11
5	24	96.0	8 10 US-09-898-887B-1	Sequence 1, App11
6	24	96.0	8 14 US-10-281-840-2	Sequence 1, App11
7	24	96.0	8 16 US-10-341-577-1	Sequence 1, App11
8	21	84.0	8 14 US-10-004-530A-4	Sequence 4, App11
9	19	76.0	8 12 US-10-182-252A-332	Sequence 322, App
10	19	76.0	8 12 US-10-182-252A-940	Sequence 940, App
11	19	76.0	8 12 US-10-182-252A-941	Sequence 941, App
12	19	76.0	8 12 US-10-182-252A-942	Sequence 942, App
13	19	76.0	8 12 US-10-182-252A-943	Sequence 943, App
14	19	76.0	8 12 US-10-182-252A-944	Sequence 944, App
15	19	76.0	8 12 US-10-182-252A-946	Sequence 946, App

16	19	76.0	8 12 US-10-182-252A-947	Sequence 947, App
17	19	76.0	8 12 US-10-182-252A-948	Sequence 948, App
18	19	76.0	8 12 US-10-182-252A-950	Sequence 950, App
19	19	76.0	8 12 US-10-182-252A-951	Sequence 951, App
20	19	76.0	8 12 US-10-182-252A-1285	Sequence 1285, App
21	18	72.0	8 9 US-09-899-422-28	Sequence 28, App1
22	18	72.0	8 9 US-09-898-234-38	Sequence 38, App1
23	18	72.0	8 9 US-09-899-429A-38	Sequence 38, App1
24	18	72.0	8 9 US-09-017-743C-100	Sequence 100, App
25	18	72.0	8 9 US-09-792-156-28	Sequence 28, App1
26	18	72.0	8 12 US-10-609-217-537	Sequence 537, App
27	18	72.0	8 12 US-10-609-217-539	Sequence 539, App
28	18	72.0	8 12 US-10-149-135-36	Sequence 36, App1
29	18	72.0	8 12 US-10-149-135-116	Sequence 116, App
30	18	72.0	8 12 US-10-149-135-313	Sequence 313, App
31	18	72.0	8 12 US-10-149-135-549	Sequence 549, App
32	18	72.0	8 12 US-10-149-135-649	Sequence 649, App
33	18	72.0	8 12 US-10-149-135-674	Sequence 674, App
34	18	72.0	8 12 US-10-149-135-808	Sequence 808, App
35	18	72.0	8 12 US-10-149-135-818	Sequence 818, App
36	18	72.0	8 12 US-10-149-135-1175	Sequence 1175, App
37	18	72.0	8 12 US-10-149-135-1180	Sequence 1180, App
38	18	72.0	8 12 US-10-149-135-1192	Sequence 1192, App
39	18	72.0	8 12 US-10-149-135-1487	Sequence 1487, App
40	18	72.0	8 12 US-10-149-135-1651	Sequence 1651, App
41	18	72.0	8 12 US-10-149-135-1763	Sequence 1763, App
42	18	72.0	8 12 US-10-149-135-1854	Sequence 1854, App
43	18	72.0	8 12 US-10-149-135-2451	Sequence 2451, App
44	18	72.0	8 12 US-10-387-957-6	Sequence 6, App11
45	18	72.0	8 12 US-10-632-388-537	Sequence 537, App

ALIGNMENTS

RESULT 1
US-09-896-903C-2
; Sequence 2, Application US/09896903C
; Publication No. US2003005023A1
; GENERAL INFORMATION:
; APPLICANT: Butman, Anand C.
; APPLICANT: Mukherjee, Rama
; APPLICANT: Prasad, Sudhanand
; APPLICANT: Jaggi, Manu
; APPLICANT: Singh, Anu T.
; TITLE OF INVENTION: PEPTIDE COMBINATION FOR TREATMENT OF CANCER
; FILE REFERENCE: 0132970
; CURRENT APPLICATION NUMBER: US/09/896,903C
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ. ID NOS.: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This peptide
; OTHER INFORMATION: was synthetically generated.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: /product = Butanoyl D-phenylalanine/label =
; OTHER INFORMATION: Butanoyl-D-phe
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: / product = alpha-Aminoisobutyric acid/label = Alb
US-09-896-903C-2
Query Match 100.0%; Score 25; DB 10; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8
|:|:|:|
DB 1 XQWAVXHL 8

RESULT 2

US-10-186-226A-2
; Sequence 2, Application US/10186226A
; Publication No. US20030105009A1
; GENERAL INFORMATION:
; APPLICANT: Mukherjee, Rudhanand
; APPLICANT: Prasad, Sudhanand
; APPLICANT: Burman, Anand C.
; APPLICANT: Mathur, Archana
; APPLICANT: Sharma, Rajan
; APPLICANT: Jaggi, Manu
; TITLE OF INVENTION: POLYPEPTIDES OF COVALENTLY LINKED SYNTHETIC BIOACTIVE PEPTIDE ANA
; TITLE OF INVENTION: FOR TREATMENT OF CANCER
; FILE REFERENCE: U 014073-7
; CURRENT APPLICATION NUMBER: US/10/186,226A
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This peptide was synthetically generated
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: /product = D-Phenylalanine/label = D-Phe
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: /product = Alpha-amino-isobutyric acid/label = Alb
US-10-186-226A-2

Query Match 100.0%; Score 25; DB 14; Length 8;
Best local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8
|:|:|:|
DB 1 XQWAVXHL 8

RESULT 3

US-10-329-321A-2
; Sequence 2, Application US/10329321A
; Publication No. US20040121950A1
; GENERAL INFORMATION:
; APPLICANT: Mukherjee, Rama
; APPLICANT: Burman, Anand
; APPLICANT: Singh, Anu
; APPLICANT: Jaggi, Manu
; APPLICANT: Prasad, Sudhanand
; APPLICANT: Dutt, Sarjana
; TITLE OF INVENTION: A DRUG COMPRISING SYNTHETIC PEPTIDE ANALOGS FOR THE TREATMENT OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: U 014319-1
; CURRENT APPLICATION NUMBER: US/10/329,321A
; CURRENT FILING DATE: 2002-12-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: This peptide was synthetically generated
; FEATURE:

; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: /product = D-phenylalanine/label = D-Phe
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: /product = 2-amino-isobutyric acid/label = Alb
US-10-329-321A-2

Query Match 100.0%; Score 25; DB 16; Length 8;
Best local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8
|:|:|:|
DB 1 XQWAVXHL 8

RESULT 4

US-09-766-347-1
; Sequence 1, Application US/09766347
; Patent No. US20020169107A1
; GENERAL INFORMATION:
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Cantrell, Gary
; APPLICANT: Achilefu, Samuel
; APPLICANT: Bugaj, Joseph
; APPLICANT: Dorehow, Richard
; APPLICANT: Mallinckrodt Inc.
; TITLE OF INVENTION: NOVEL AROMATIC AZIDES FOR TYPE I PHOTOTHERAPY
; FILE REFERENCE: MRD-60
; CURRENT APPLICATION NUMBER: US/09/766,347
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent In Version 3.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(8)
; OTHER INFORMATION: Bombesin analog
US-09-766-347-1

Query Match 96.0%; Score 24; DB 9; Length 8;
Best local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHL 8
|:|:|:|
DB 1 QWAVGHL 7

RESULT 5

US-09-898-887B-1
; Sequence 1, Application US/0989887B
; Publication No. US20030158127A1
; GENERAL INFORMATION:
; APPLICANT: Mallinckrodt Inc.
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Cantrell, Gary
; APPLICANT: Achilefu, Samuel I.
; APPLICANT: Bugaj, Joseph
; APPLICANT: Dorehow, Richard
; TITLE OF INVENTION: AROMATIC SULFONATES FOR TYPE I PHOTOTHERAPY
; FILE REFERENCE: MRD-61
; CURRENT APPLICATION NUMBER: US/09/898,887B
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 8

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The sulfenyl-bombesin (7-14) conjugate has the following
OTHER INFORMATION: molecular structure:
OTHER INFORMATION: p-azidotetrafluorobenzoyl-Gln-Trp-Ala-Val-Gly-His-Leu-Met-NH₂.
US-09-898-887B-1

Query Match 96.0%; Score 24; DB 10; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHL 8
 |:::|
DB 1 QMAVGH 7

RESULT 6
US-10-281-840-2
Sequence 2, Application US/10281840
Publication No. US20030082192A1
GENERAL INFORMATION:
APPLICANT: Safaay, Ahmad
TITLE OF INVENTION: Multidrug Multiligand Conjugates for Targeted Drug Delivery
FILE REFERENCE: P66788US01GP
CURRENT APPLICATION NUMBER: US/10/281,840
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US 60/348,299
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-281-840-2

Query Match 96.0%; Score 24; DB 14; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHL 8
 |:::|
DB 1 QMAVGH 7

RESULT 7
US-10-341-577-1
Sequence 1, Application US/10341577
Publication No. US20040136906A1
GENERAL INFORMATION:
APPLICANT: Bracco Research U.S.A.
TITLE OF INVENTION: Improved Gastrin Releasing Peptide Compounds
FILE REFERENCE: 57637-1020
CURRENT APPLICATION NUMBER: US/10/341,577
CURRENT FILING DATE: 2003-01-13
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: This peptide is the receptor
OTHER INFORMATION: binding site of bombesin and is also known as BEN(7-14)
US-10-341-577-1

Query Match 96.0%; Score 24; DB 16; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHL 8
 |:::|

DB 1 QMAVGH 7

RESULT 8
US-10-004-530A-4
Sequence 4, Application US/10004530A
Publication No. US20030050436A1
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Moreau, Jacques-Pierre
APPLICANT: Kim, Sun H.
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
FILE REFERENCE: 00537-00900K
CURRENT APPLICATION NUMBER: US/10/004,530A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/260,846
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: 08/337,127
PRIOR FILING DATE: 1994-11-10
PRIOR APPLICATION NUMBER: 07/779,039
PRIOR FILING DATE: 1991-10-18
PRIOR APPLICATION NUMBER: 07/502,438
PRIOR FILING DATE: 1990-03-30
PRIOR APPLICATION NUMBER: 07/397,169
PRIOR FILING DATE: 1989-08-21
PRIOR APPLICATION NUMBER: 07/376,555
PRIOR FILING DATE: 1989-07-07
PRIOR APPLICATION NUMBER: 07/317,941
PRIOR FILING DATE: 1989-03-02
PRIOR APPLICATION NUMBER: 07/282,328
PRIOR FILING DATE: 1988-12-09
PRIOR APPLICATION NUMBER: 07/257,998
PRIOR FILING DATE: 1988-10-14
PRIOR APPLICATION NUMBER: 07/248,771
PRIOR FILING DATE: 1988-09-23
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated peptide
FEATURE:
NAME/KEY: VARIANT
LOCATION: 8
OTHER INFORMATION: Xaa = statine;
US-10-004-530A-4

Query Match 84.0%; Score 21; DB 14; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.2e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QXXVXHL 7
 |:::|
DB 1 EQMAVGH 7

RESULT 9
US-10-182-252A-322
Sequence 322, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
FILE REFERENCE: 030307/0205

```
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-322

Query Match
Best Local Similarity 76.0%; Score 19; DB 12; Length 8;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
Db 1 QIGIPH 6

RESULT 10
US-10-182-252A-940
; Sequence 940, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-940

Query Match
Best Local Similarity 76.0%; Score 19; DB 12; Length 8;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
Db 1 QIGIPH 6

RESULT 11
US-10-182-252A-941
; Sequence 941, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
```

```
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-941

Query Match
Best Local Similarity 76.0%; Score 19; DB 12; Length 8;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
Db 1 QIGIPH 6

RESULT 12
US-10-182-252A-942
; Sequence 942, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-942

Query Match
Best Local Similarity 76.0%; Score 19; DB 12; Length 8;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
```

Db 1 QIGIPH 6

RESULT 13

US-10-182-252A-943
 ; Sequence 943, Application US/10182252A
 ; Publication No. US20040072162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FOMSGAARD, ANDERS
 ; APPLICANT: BRUNAK, SOREN
 ; APPLICANT: BUUS, SOREN
 ; APPLICANT: CORBET, SYLVIE
 ; APPLICANT: LAUEMOLLER, SANNE LISE
 ; APPLICANT: HANSEN, JAN
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
 ; FILE REFERENCE: 030307/0205
 ; CURRENT APPLICATION NUMBER: US/10/182,252A
 ; PRIOR FILING DATE: 2003-04-10
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059
 ; PRIOR FILING DATE: 2001-01-29
 ; PRIOR APPLICATION NUMBER: EP 00610017.6
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US 60/179,333
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 1388
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 943
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
 US-10-182-252A-943

Query Match 76.0%; Score 19; DB 12; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
 Db 1 QIGIPH 6

RESULT 14
 US-10-182-252A-944
 ; Sequence 944, Application US/10182252A
 ; Publication No. US20040072162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FOMSGAARD, ANDERS
 ; APPLICANT: BRUNAK, SOREN
 ; APPLICANT: BUUS, SOREN
 ; APPLICANT: CORBET, SYLVIE
 ; APPLICANT: LAUEMOLLER, SANNE LISE
 ; APPLICANT: HANSEN, JAN
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
 ; FILE REFERENCE: 030307/0205
 ; CURRENT APPLICATION NUMBER: US/10/182,252A
 ; PRIOR FILING DATE: 2003-04-10
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059
 ; PRIOR FILING DATE: 2001-01-29
 ; PRIOR APPLICATION NUMBER: EP 00610017.6
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US 60/179,333
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 1388
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 944
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
 US-10-182-252A-944

Query Match 76.0%; Score 19; DB 12; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
 Db 1 QIGIPH 6

RESULT 15
 US-10-182-252A-946
 ; Sequence 946, Application US/10182252A
 ; Publication No. US20040072162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FOMSGAARD, ANDERS
 ; APPLICANT: BRUNAK, SOREN
 ; APPLICANT: BUUS, SOREN
 ; APPLICANT: CORBET, SYLVIE
 ; APPLICANT: LAUEMOLLER, SANNE LISE
 ; APPLICANT: HANSEN, JAN
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
 ; FILE REFERENCE: 030307/0205
 ; CURRENT APPLICATION NUMBER: US/10/182,252A
 ; PRIOR FILING DATE: 2003-04-10
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059
 ; PRIOR FILING DATE: 2001-01-29
 ; PRIOR APPLICATION NUMBER: EP 00610017.6
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US 60/179,333
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 1388
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 946
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
 US-10-182-252A-946

Query Match 76.0%; Score 19; DB 12; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
 Db 1 QIGIPH 6

RESULT 16
 US-10-182-252A-947
 ; Sequence 947, Application US/10182252A
 ; Publication No. US20040072162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FOMSGAARD, ANDERS
 ; APPLICANT: BRUNAK, SOREN
 ; APPLICANT: BUUS, SOREN
 ; APPLICANT: CORBET, SYLVIE
 ; APPLICANT: LAUEMOLLER, SANNE LISE
 ; APPLICANT: HANSEN, JAN
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
 ; FILE REFERENCE: 030307/0205
 ; CURRENT APPLICATION NUMBER: US/10/182,252A
 ; PRIOR FILING DATE: 2003-04-10
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059
 ; PRIOR FILING DATE: 2001-01-29
 ; PRIOR APPLICATION NUMBER: EP 00610017.6

```
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 947
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-947
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db       1 QMGIPH 6
```

```
RESULT 17
US-10-182-252A-948
; Sequence 948, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUTS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEWOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 948
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-948
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db       1 QMGIPH 6
```

```
RESULT 18
US-10-182-252A-950
; Sequence 950, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUTS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEWOLLER, SANNE LISE
```

```
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 950
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-950
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db       1 QMGIPH 6
```

```
RESULT 19
US-10-182-252A-951
; Sequence 951, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUTS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEWOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 951
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-951
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db       1 QMGIPH 6
```

```
RESULT 20
```

US-10-182-252A-1285
; Sequence 1285, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/1179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-182-252A-1285
Query Match 76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 2 QXXVXH 7
DB 1 QLGIPH 6
RESULT 21
US-09-899-422-28
; Sequence 28, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Foggy, Ingrid
; APPLICANT: Stralow, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: TNF-BP tryptic
; OTHER INFORMATION: Cleavage peptide
US-09-899-422-28

Query Match 72.0%; Score 18; DB 9; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 XVXHL 8
DB 1 LVPHL 5
RESULT 22
US-09-898-234-28
; Sequence 28, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Foggy, Ingrid
; APPLICANT: Stralow, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: TNF-BP tryptic
; OTHER INFORMATION: Cleavage peptide
US-09-898-234-28
Query Match 72.0%; Score 18; DB 9; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 XVXHL 8
DB 1 LVPHL 5
RESULT 23
US-09-899-429A-38
; Sequence 38, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Foggy, Ingrid
; APPLICANT: Stralow, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-U
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01

PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TNF-BP tryptic
OTHER INFORMATION: cleavage peptide
US-09-429A-38

Query Match
Best Local Similarity 72.0%; Score 18; DB 9; Length 8;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 XYXHL 8
:|:|
Db 1 LVPHL 5

RESULT 24
US-09-017-743C-100
Sequence 100, Application US/09017743C
Patent No. US20020177694A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
Sidney, John
Southwood, Scott
TITLE OF INVENTION: HLA Binding Peptides and Their
Uses
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3634
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,743C
FILING DATE: 03-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/590,298
FILING DATE: 23-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018623-008050US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-017-743C-100

Query Match
Best Local Similarity 72.0%; Score 18; DB 9; Length 8;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XYXHL 8
:|:|
Db 1 LVPHL 6

RESULT 25
US-09-792-356-28
Sequence 28, Application US/09792356
Publication No. US20020183485A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
Maurel-Fosy, Ingrid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
TITLE OF INVENTION: Them
FILE REFERENCE: 98,385-G
CURRENT APPLICATION NUMBER: US/09/792,356
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 08/477,639
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TNF-BP tryptic
OTHER INFORMATION: cleavage peptide
US-09-792-356-28

Query Match
Best Local Similarity 72.0%; Score 18; DB 9; Length 8;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 XYXHL 8
:|:|
Db 1 LVPHL 5

RESULT 26
US-10-609-217-537
Sequence 537, Application US/10609217
Publication No. US20040044188A1
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/609,217
CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patentin version 3.1

SEQ ID NO 537
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE
US-10-609-217-537

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 XXVHL 8
Db 1 KVFHL 5

RESULT 27
US-10-609-217-539
Sequence 539, Application US/10609217
Publication No. US2004004188A1
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-PA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/609,217
CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 539
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE
US-10-609-217-539

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVHL 8
Db 3 FHLHL 8

RESULT 28
US-10-149-135-36
Sequence 36, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Eteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE REFERENCE: 2060 0130001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298

PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-36

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVHL 8
Db 2 VPLSHL 7

RESULT 29
US-10-149-135-116
Sequence 116, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Eteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE REFERENCE: 2060 0130001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 116
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-116

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;

Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXHL 8
Db 3 VPISHL 8

RESULT 30
US-10-149-135-313
; Sequence 313, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 313
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-313

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXHL 8
Db 3 DPIGHL 8

RESULT 31
US-10-149-135-549
; Sequence 549, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US/10/149,135

CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 549
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-549

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXHL 8
Db 3 VPISHL 8

RESULT 32
US-10-149-135-649
; Sequence 649, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 649
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide

US-10-149-135-649

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
: : : : :
DB 2 VPISHL 7

RESULT 33

US-10-149-135-674

Sequence 674, Application US/10149135
Publication No. US20040053822A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Celis, Bateban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0130001

CURRENT APPLICATION NUMBER: US/10/149,135

CURRENT FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: PCT/US00/33545

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,298

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 09/189,702

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04

PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04

PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05

NUMBER OF SEQ ID NOS: 2479

SOFTWARE: PatentIn version 3.1

SEQ ID NO 674

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificial Peptide

US-10-149-135-674

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
: : : : :
DB 3 DPIGHL 8

RESULT 34

US-10-149-135-808

Sequence 808, Application US/10149135
Publication No. US20040053822A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Celis, Bateban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0130001

CURRENT APPLICATION NUMBER: US/10/149,135

CURRENT FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: PCT/US00/33545

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,298

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 09/189,702

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04

PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04

PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05

NUMBER OF SEQ ID NOS: 2479

SOFTWARE: PatentIn version 3.1

SEQ ID NO 808

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificial Peptide

US-10-149-135-808

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
: : : : :
DB 1 VPISHL 6

RESULT 35

US-10-149-135-818

Sequence 818, Application US/10149135
Publication No. US20040053822A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Celis, Bateban

APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0130001

CURRENT APPLICATION NUMBER: US/10/149,135

CURRENT FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: PCT/US00/33545

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,298

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 09/189,702

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04

PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04

PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05

NUMBER OF SEQ ID NOS: 2479

SOFTWARE: PatentIn version 3.1

SEQ ID NO 818

LENGTH: 8

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-818

Query Match
Best Local Similarity 72.0%; Score 18; DB 12; Length 8;
                          33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
   :|:|:|
Db 1 DPLGHL 6

RESULT 36
US-10-149-135-1175
; Sequence 1175, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1175
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1175

Query Match
Best Local Similarity 72.0%; Score 18; DB 12; Length 8;
                          33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
   :|:|:|
Db 1 VPISHL 6

RESULT 37
US-10-149-135-1180
; Sequence 1180, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
```

```
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1180
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1180

Query Match
Best Local Similarity 72.0%; Score 18; DB 12; Length 8;
                          33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
   :|:|:|
Db 2 VPISHL 7

RESULT 38
US-10-149-135-1192
; Sequence 1192, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
```

```

; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1192
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1192

Query Match      72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 XXVXHL 8
       :|:|:|
Db      1 DPIGHL 6

RESULT 39
US-10-149-135-1487
; Sequence 1487, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Bstedan
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1487
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1487

Query Match      72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 XXVXHL 8
       :|:|:|
Db      2 VPISHL 7

RESULT 40
US-10-149-135-1651
; Sequence 1651, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Bstedan
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1651

Query Match      72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 XXVXHL 8
       :|:|:|
Db      2 DPIGHL 7

RESULT 41
US-10-149-135-1763
; Sequence 1763, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Bstedan
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1763
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PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1763
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-1763

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 2 VPISHL 7

RESULT 42
US-10-149-135-1854
Sequence 1854, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikee, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Basteen
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0130001
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1854
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-1854

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 2 DPIGHL 7

RESULT 43
US-10-149-135-2451
Sequence 2451, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikee, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Basteen
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0130001
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2451
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-2451

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 1 PPISHL 6

RESULT 44
US-10-387-957-6
Sequence 6, Application US/10387957
Publication No. US20040052809A1
GENERAL INFORMATION:
APPLICANT: Glaxosmithkline Biologicals s.a.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45284
CURRENT APPLICATION NUMBER: US/10/387,957
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-387-957-6

Query Match 72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7

Db 1 MCGYMKH 7

RESULT 45
 US-10-632-388-537
 ; Sequence 537, Application US/10632388
 ; Publication No. US20040053845A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FEIGE, ULRICH
 ; APPLICANT: LIU, CHUAN-PA
 ; APPLICANT: CHEETHAM, JANET C.
 ; APPLICANT: BOONE, THOMAS CHARLES
 ; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 ; FILE REFERENCE: A-527
 ; CURRENT APPLICATION NUMBER: US/10/632,388
 ; CURRENT FILING DATE: 2003-07-31
 ; PRIOR APPLICATION NUMBER: US/09/428,082B
 ; PRIOR FILING DATE: 1999-10-22
 ; PRIOR APPLICATION NUMBER: 60/105,371
 ; PRIOR FILING DATE: 1998-10-23
 ; NUMBER OF SEQ ID NOS: 113
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 537
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE
 US-10-632-388-537

Query Match 72.0%; Score 18; DB 12; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.2e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 XVXHL 8
 Db 1 KVFHL 5

Search completed: August 19, 2004, 16:00:18
 Job time : 38 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 19, 2004, 15:47:57 ; Search time 11.5 Seconds
(without alignments)
66.916 Million cell updates/sec

Title: VARIANT1
Perfect score: 25
Sequence: 1 XQXXVXHL 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 148

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	60.0	8	2	A61496 ubiquitin - celery
2	13	52.0	8	2	SS3008 citrate synthase -
3	12	48.0	8	2	PT0368 Ig gamma chain C r
4	11	44.0	8	2	A31570 angiotensin-conver
5	10	40.0	8	2	T14906 hypochlorite prote
6	10	40.0	8	2	PH1618 Ig H chain V-D-J r
7	10	40.0	8	2	A42689 major postsynaptic
8	10	40.0	8	2	PC4372 telomeric and tetr
9	10	40.0	8	2	B47594 aspartate kinase (
10	9	36.0	8	2	XGHUEU urine glycopeptide
11	9	36.0	8	2	S43971 tumor-associated a
12	9	36.0	8	2	S43972 tumor-associated a
13	9	36.0	8	2	T10077 hypochlorite prote
14	9	36.0	8	2	S68802 nitrate reductase
15	9	36.0	8	2	PQ0726 unidentified 4.5/4
16	9	36.0	8	2	JS0316 leucokinin VI - Ma
17	9	36.0	8	2	PT0298 Ig heavy chain CRD
18	9	36.0	8	2	B45800 serum albumin - do
19	9	36.0	8	2	AS4823 olfactory receptor
20	9	36.0	8	2	BS4823 cytochrome-c oxida
21	9	36.0	8	2	S65381 ferredoxin a2 - Ja
22	9	36.0	8	2	A25836 l-serine ammonia-1
23	9	36.0	8	2	B24749 neuropeptide B - b
24	8	32.0	8	2	S19288 acylase - Kluyvera
25	8	32.0	8	2	S70727 1pgf protein - Shi
26	8	32.0	8	2	S63493 dissimilatory sulf
27	8	32.0	8	2	PA0035 protein QA300039 -
28	8	32.0	8	2	TI0952 hypochlorite prote
29	8	32.0	8	2	TI0952

30	8	32.0	8	2	S78036 ribosomal protein
31	8	32.0	8	2	PT0030 inulinase (EC 3.2.
32	8	32.0	8	2	PL0162 paramyosin - north
33	8	32.0	8	2	A46306 spasmogenic toxin
34	8	32.0	8	2	A14683 aspartate transami
35	8	32.0	8	2	PT0323 Ig heavy chain CRD
36	8	32.0	8	2	PN0043 phosphatidylethano
37	8	32.0	8	2	I49404 prealbumin - weste
38	8	32.0	8	2	C39690 neutral cell adhesi
39	8	32.0	8	2	A35180 neutral proteinase
40	8	32.0	8	2	S29272 tocopherol-binding
41	7	28.0	8	2	A61348 red pigment-concen
42	7	28.0	8	2	A28004 adipokinetic hormo
43	7	28.0	8	2	S08995 hypertrehalosemic
44	7	28.0	8	2	S08996 hypertrehalosemic
45	7	28.0	8	2	S10596 adipokinetic hormo

ALIGNMENTS

RESULT 1
A61496
ubiquitin - celery (fragment)
C:Species: Apium graveolens (celery)
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
C:Accession: A61496
R:Goldstein, G.; Scheid, M.; Hammerling, U.; Boyse, E.A.; Schleisner, D.H.; Niall, H.D.
Proc. Natl. Acad. Sci. U.S.A. 72, 11-15, 1975
A:Title: Isolation of a polypeptide that has lymphocyte-differentiating properties and is
A:Reference number: A61496; MUID:75120426; PMID:1078892
A:Accession: A61496
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <GOL>
A>Note: a small amount of material was sequenced; the amino-terminal residue is unlikely

Query Match 60.0%; Score 15; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 2.8e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XQXXVXHL 8
Db 1 XQIXVXKL 8

RESULT 2
S53008
citrate synthase - cucurbit
C:Species: Cucurbita sp. (cucurbit)
C>Date: 14-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C:Accession: S53008
R:Kato, A.; Hayashi, M.; Mori, H.; Nishimura, M.
Plant Mol. Biol. 27, 377-390, 1995
A:Title: Molecular characterization of a glyoxysomal citrate synthase that is synthesized
A:Reference number: S53007; MUID:95195164; PMID:7888626
A:Accession: S53008
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <KAT>

Query Match 52.0%; Score 13; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXXVX 6
Db 2 AQTMTA 7

RESULT 3
PT0368
Ig gamma chain C region (gamma-1) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-1996
 C:Accession: P0368
 R:Millili, M.; Fougereau, M.; Gaglielmi, P.; Schiff, C.
 M.J. Immunol. 28, 753-761, 1991
 A:Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.
 A:Reference number: P0368; MWID:91312348; PMID:1506961
 A:Accession: P0368
 A:Molecule type: mRNA
 A:Residues: 1-8 <ML>
 A:Experimental source: fetal liver
 C:Keywords: immunoglobulin

Query Match 48.0%; Score 12; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXV 6
 :|:|:
 DB 2 HQGP 7

RESULT 4

A31570
 angiotensin-converting enzyme inhibitor - yellowfin tuna
 C:Species: Thunnus albacares (yellowfin tuna)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000
 C:Accession: A31570
 R:Kohma, Y.; Matsunoto, S.; Oka, H.; Terramoto, T.; Okabe, M.; Mimura, T.
 Biochem. Biophys. Res. Commun. 155, 332-337, 1988
 A:Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.
 A:Reference number: A31570; MWID:88326322; PMID:3415688
 A:Accession: A31570
 A:Molecule type: protein
 A:Residues: 1-8 <KH>
 A:Note: the source is designated as Neothunnus macropterus
 C:Superfamily: unassigned animal peptides
 C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 44.0%; Score 11; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHL 8
 :|:
 DB 2 TH 4

RESULT 5

T14906
 hypothetical protein - parsley
 C:Species: Petroselinum crispum (parsley)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T14906
 R:Feidtrugge, W.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Harter, K.; Weishaar, B.
 Plant Cell 6, 1607-1621, 1994
 A:Title: Functional analysis of a light-responsive plant bZIP transcriptional regulator.
 A:Reference number: T14906; MWID:95128172; PMID:7827494
 A:Accession: T14906
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-8 <FL>
 A:Cross-references: EMBL:575395; NID:9913201; PID:el94245

Query Match 40.0%; Score 10; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXH 7
 :|:|:
 DB 1 MKH 3

RESULT 6

PH618
 Ig H chain V-D-J region (clone B-1ees 33) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH618
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-1ees mice
 A:Reference number: PH1580; MWID:93301609; PMID:8315387
 A:Accession: PH618
 A:Molecule type: DNA
 A:Residues: 1-8 <LE>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 40.0%; Score 10; DB 2; Length 8;
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 VXH 7
 :|:|:
 DB 1 CARH 4

RESULT 7

A42689
 major postsynaptic density protein - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 26-May-1994
 C:Accession: A42689
 R:Wu, K.; Huang, Y.; Adler, J.; Black, I.B.
 Proc. Natl. Acad. Sci. U.S.A. 89, 3015-3019, 1992
 A:Title: On the identity of the major postsynaptic density protein.
 A:Reference number: A42689; MWID:92212958; PMID:1313576
 A:Accession: A42689
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <WU>

Query Match 40.0%; Score 10; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
 :|:|:
 DB 2 LKVPNT 7

RESULT 8

PC4372
 telomeric and tetraplex DNA binding protein qTBP42 II - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
 C:Accession: PC4372
 R:Farig, G.; Weisman-Shomer, P.; Fry, M.
 Biochem. Biophys. Res. Commun. 237, 617-623, 1997
 A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CAI
 A:Reference number: PC4372; MWID:97445086; PMID:9299414
 A:Accession: PC4372
 A:Molecule type: protein
 A:Residues: 1-8 <SR>
 A:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular
 F/3-8/Domain: RNP2 #status predicted <RNP>

Query Match 40.0%; Score 10; DB 2; Length 8;
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 OXXVXHL 8
 :|:|:
 DB 1 KXFGGL 7

RESULT 9

B47594

aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)

C/Species: Corynebacterium flavum
C/Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997

C/Accession: B47594

R/Polletie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.

J. Bacteriol. 175, 4096-4103, 1993

A/Title: Gene structure and expression of the Corynebacterium flavum N13 ask-ase operon.

A/Reference number: A47594; MUID:93308089; PMID:8100567

A/Status: preliminary; not compared with conceptual translation

A/Accession: B47594

A/Molecule type: DNA

A/Residues: 1-8 <FOL>

C/Keywords: phosphotransferase

Query Match 40.0%; Score 10; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 2.8e+05;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXV 6

Db 1 MEBAVL 6

RESULT 10

XGHUEU

urine glycopeptide - human

C/Species: Homo sapiens (man)

C/Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C/Accession: A03188

R/Note, C.J.; Weiss, J.B.

Biochem. J. 123, 25P, 1971

A/Title: Identification in urine of a low-molecular-weight polar glycopeptide containing

A/Reference number: A03188; MUID:72062338; PMID:5126885

A/Accession: A03188

A/Molecule type: protein

A/Residues: 1-8 <LOT>

C/Comment: The identity of the glycoprotein from which this peptide is derived is unknown

re has also been found (see PIR:XGHUE).

C/Superfamily: unassigned animal peptides

C/Keywords: glycoprotein

F/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 36.0%; Score 9; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7

Db 2 EH 3

RESULT 11

S43971

tumor-associated antigen MUT1 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000

C/Accession: S43971

R/Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.

Nature 369, 67-71, 1994

A/Title: CTL induction by a tumor-associated antigen octapeptide derived from a murine

A/Reference number: S43971; MUID:94217811; PMID:8164742

A/Accession: S43971

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-8 <MAN>

C/Superfamily: unassigned animal peptides

Query Match 36.0%; Score 9; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXV 6

Db 2 EQNTAQ 7

RESULT 12

S43972

tumor-associated antigen MUT2 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000

C/Accession: S43972

R/Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.

Nature 369, 67-71, 1994

A/Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine

A/Reference number: S43971; MUID:94217811; PMID:8164742

A/Accession: S43972

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-8 <MAN>

C/Superfamily: unassigned animal peptides

Query Match 36.0%; Score 9; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXV 6

Db 2 EQNTAQ 7

RESULT 13

T10077

hypothetical protein N - Methylophilus methylotrophus (fragment)

C/Species: Methylophilus methylotrophus

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C/Accession: T10077

R/Chistoserdov, A.Y.; McIntire, W.S.; Mathews, F.S.; Lidstrom, M.E.

J. Bacteriol. 176, 4073-4080, 1994

A/Title: Organization of the methylamine utilization (mau) genes in Methylophilus methyl-

A/Reference number: Z16936; MUID:94292427; PMID:8021188

A/Accession: T10077

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-8 <CHT>

A/Cross-references: EMBL:Z16407; NID:G561931; PIDN:AAB4655.1; PID:G561933

A/Experimental source: strain W3A1

C/Genetics:

A/Gene: mauN

Query Match 36.0%; Score 9; DB 2; Length 8;
Best Local Similarity 20.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXV 5

Db 4 LQAIL 8

RESULT 14

S68802

nitrate reductase (NADH) inhibitor - spinach (fragment)

C/Species: Spinacia oleracea (spinach)

C/Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998

C/Accession: S68802

R/Bachmann, M.; Huber, J.L.; Liao, P.C.; Gage, D.A.; Huber, S.C.

FEBS Lett. 387, 127-131, 1996

A/Title: The inhibitor protein of phosphorylated nitrate reductase from spinach (Spinach)

A/Reference number: S68802; MUID:96244508; PMID:8674533

A/Accession: S68802

A/Molecule type: protein

A/Residues: 1-8 <BAC>

A/Experimental source: leaves; strain cv. Bloomsdale

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 20.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 XXVXH 7
 :|:|:
 Db 3 LSVAY 7

RESULT 15
 P00726
 unidentified 4.5/45K [imported] - rice (fragment)
 C/Species: Oryza sativa (rice)
 C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C/Accession: P00726
 R/Komatsu, S.; Kajiwara, H.; Hirano, H.
 Theor. Appl. Genet. 86, 935-942, 1993
 A/Title: A rice protein library; a data-file of rice proteins separated by two-dimension
 A/Reference number: P00696
 A/Accession: P00726
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-8 <KOM>

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 X0XXVX 6
 :|:|:
 Db 2 V00DAA 7

RESULT 16
 JS0316
 leucokinin VI - Madeira cockroach
 C/Species: Leucophaea maderae (Madeira cockroach)
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C/Accession: JS0316
 R/Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 27-30, 1987
 A/Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic
 A/Reference number: JS0315
 A/Accession: JS0316
 A/Molecule type: protein
 A/Residues: 1-8 <HO>
 C/Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act
 C/Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid
 F/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
 F/8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7
 :|:
 Db 4 FH 5

RESULT 17
 PT0298
 Ig heavy chain CRD3 region (clone 5-103A) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0298
 R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
 A/Reference number: PT0222; MWID:91108337; PMID:1899102
 A/Accession: PT0298
 A/Molecule type: DNA

A/Residues: 1-8 <YAM>
 A/Experimental source: B lymphocyte
 C/Keywords: heterotrimer; immunoglobulin
 Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 28.6%; Pred. No. 2.8e+05;
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 QXXVXHL 8
 :|:|:
 Db 1 RMTVVVL 7

RESULT 18
 B45800
 serum albumin - dog (fragment)
 C/Species: Canis lupus familiaris (dog)
 C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 31-Dec-1993
 C/Accession: B45800
 R/Carraway, R.E.; Cochran, D.E.; Boucher, W.; Mltira, S.P.
 J. Immunol. 143, 1680-1684, 1989
 A/Title: Structures of histamine-releasing peptides formed by the action of acid protease
 A/Reference number: A45800; MWID:89341406; PMID:2474609
 A/Accession: B45800
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-8 <CAR>

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7
 :|:
 Db 4 RH 5

RESULT 19
 A54823
 olfactory receptor I7 - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C/Accession: A54823
 R/Chess, A.; Simon, I.; Cedar, H.; Axel, R.
 Cell 78, 823-834, 1994
 A/Title: Allelic inactivation regulates olfactory receptor gene expression.
 A/Reference number: A54823; MWID:94373818; PMID:8087849
 A/Accession: A54823
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-8 <CHE>

Query Match 36.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7
 :|:
 Db 5 NH 6

RESULT 20
 B54823
 olfactory receptor I7 - western wild mouse (fragment)
 C/Species: Mus spretus (western wild mouse)
 C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C/Accession: B54823
 R/Chess, A.; Simon, I.; Cedar, H.; Axel, R.
 Cell 78, 823-834, 1994
 A/Title: Allelic inactivation regulates olfactory receptor gene expression.
 A/Reference number: A54823; MWID:94373818; PMID:8087849
 A/Accession: B54823
 A/Status: preliminary

A:Molecule type: DNA
A:Residues: 1-8 <CHE>

Query Match 36.0%; Score 9; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7
DB 5 NH 6

RESULT 21

S65381

Cytochrome-c oxidase (EC 1.9.3.1) chain VIIb, hepatic - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C:Accession: S65381

R:Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term

A:Reference number: S65372; MUID:95324523; PMID:7601105

A:Accession: S65381

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <SCH>

C:Keywords: oxidoreductase

Query Match 36.0%; Score 9; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVX 6
DB 1 QNXLD 5

RESULT 22

S69165

Ferredoxin a2 - Japanese radish (fragment)

C:Species: Kaiware daikon (Japanese radish)

C:Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998

C:Accession: S69165

R:Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.

Arch. Biochem. Biophys. 316, 797-802, 1995

A:Title: Four ferredoxins from Japanese radish leaves.

A:Reference number: S69164; MUID:95168867; PMID:7864635

A:Accession: S69165

A:Molecule type: protein

A:Residues: 1-8 <OBA>

C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 36.0%; Score 9; DB 2; Length 8;
Best Local Similarity 20.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXV 5
DB 4 EEDIV 8

RESULT 23

A25836

L-serine ammonia-lyase (EC 4.3.1.17) - Escherichia coli (fragment)

C:Species: Escherichia coli

C:Date: 24-Jan-1988 #sequence_revision 24-Jan-1988 #text_change 21-Jun-2002

C:Accession: A25836

R:Heinicz, M.C.; McFall, E.

J. Bacteriol. 123, 1163-1168, 1975

A:Title: N-terminal amino acid sequences of D-serine deaminases of wild-type and operat

A:Reference number: A25836; MUID:76005414; PMID:1099073

A:Contents: K12

A:Accession: A25836

A:Molecule type: protein
A:Residues: 1-8 <HEI>

Query Match 36.0%; Score 9; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7
DB 6 RH 7

RESULT 24

B24749

neuropeptide B - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000

C:Accession: B24749

R:Yang, H.Y.T.; Fracta, W.; Majane, E.A.; Costa, E.

Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985

A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b

A:Reference number: A94074; MUID:86067985; PMID:3865193

A:Accession: B24749

A:Molecule type: protein

A:Residues: 1-8 <YAN>

C:Superfamily: unassigned animal peptides

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
DB 3 FQPO 6

RESULT 25

S19288

acylase - Kluverera cryocrescens

C:Species: Kluverera cryocrescens

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S19288

R:Martin, U.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.

Biochem. J. 280, 653-662, 1991

A:Title: Chemical modification of serine at the active site of penicillin acylase from K

A:Reference number: S19288; MUID:92109664; PMID:1764029

A:Accession: S19288

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <MAR>

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVX 6
DB 1 CNMHWI 6

RESULT 26

S70727

lgf protein - Shigella flexneri (fragment)

C:Species: Shigella flexneri

C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999

C:Accession: S70727

R:Alaoui, A.; Sansonetti, P.J.; Menard, R.; Barzu, S.; Mounier, J.; Phalipou, A.; Parot

Mol. Microbiol. 17, 461-470, 1995

A:Title: Mxlg, a membrane protein required for secretion of Shigella spp. Tpa invasins: 1

A:Reference number: S70727; MUID:96100445; PMID:8559065

A:Accession: S70727

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-8 <ALT>
 A:Cross-references: EMBL:248957; NID:92929880; PID:CAA8821.1; PID:92929881
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995
 C:Genetics:
 A:Gene: 199F

Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
 :||:
 DB 2 KQNN 5

RESULT 27

S63493

disimilatory sulfite reductase gamma chain, membrane-bound and soluble - Desulfovibrio

C:Species: Desulfovibrio desulfuricans

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S63493; S63494

R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.

Bur. J. Biochem. 233, 873-879, 1995

A>Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio

A:Reference number: S63489; MUID:96085152; PMID:8521853

A:Accession: S63493

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <STE>

A:Accession: S63494

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <ST2>

Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;
 Matches 0; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7
 :||:
 DB 1 AEITY 5

RESULT 28

PA0035

protein QA300039 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997

C:Accession: PA0035

R:Kamo, M.; Kawakami, T.; Miyake, N.; Tsugita, A.

submitted to JIPID, July 1994

A>Description: Separation and characterization of Arabidopsis proteins by two-dimensions

A:Reference number: PA0001

A:Accession: PA0035

A:Molecule type: protein

A:Residues: 1-8 <KAM>

A:Experimental source: stem

Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
 :||:
 DB 1 LQXD 4

RESULT 29

T10952

hypothetical protein 1 - spring vetch
 , C:Species: Vicia sativa (spring vetch, tare)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: T10952
 R:Christiansen, A.; Hansen, A.C.; Viññ, I.; Pallisgaard, N.; Larsen, K.; Yang, W.C.; Biese

submitted to the EMBL Data Library, December 1995

A>Description: A novel type of DNA binding protein interacts with a conserved sequence in

A:Reference number: Z17228

A:Accession: T10952

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-8 <CHR>

A:Cross-references: EMBL:X95995; NID:g1360633; PID:e225824

Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 :||:
 DB 2 MMTLVS 7

RESULT 30

S78036

ribosomal protein Yms-B, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)

C:Species: Saccharomyces cerevisiae

C>Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997

C:Accession: S78036

R:Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Witmar

Bur. J. Biochem. 245, 449-456, 1997

A>Title: Identification and characterization of the genes for mitochondrial ribosomal pr

A:Reference number: S78018; MUID:97296414; PMID:9151578

A:Accession: S78036

A:Molecule type: protein

A:Residues: 1-8 <KTP>

C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 :||:
 DB 1 MNXXVD 6

RESULT 31

PT0030

inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)

N:Alternate names: inulase

C:Species: Aspergillus ficuum

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999

C:Accession: PT0030

R:Etalibi, M.; Baratt, J.C.

Agric. Biol. Chem. 54, 61-68, 1990

A>Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.

A:Reference number: PT0030; MUID:90344234; PMID:1368526

A:Accession: PT0030

A:Molecule type: protein

A:Residues: 1-8 <ETP>

C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 Query Match 32.0%; Score 8; DB 2; Length 8;
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
 :||:
 DB 4 DQPY 7

RESULT 32

PL0162

paramyosin - northern quahog (fragment)

C/Species: Mercenaria mercenaria (northern quahog)
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 11-May-2000
C/Accession: PL0162
R/Matabe, S.; Teuchiya, T.; Hartshorne, D.J.
Comp. Biochem. Physiol. B 94, 813-821, 1989
A/Title: Phosphorylation of paramyosin.
A/Reference number: PL0162; MUID:90107385; PMID:2532591
A/Accession: PL0162
A/Molecule type: protein
A/Residues: 1-8 <MAT>
A/Experimental source: white adductor muscle
A/Note: The sequence is the phosphorylated tryptic peptide
C/Comment: This protein is thought to exist as a dimer of two subunits, termed alpha-par
C/Keywords: muscle; phosphoprotein
P/5/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXX 6
: : :
Db 2 RMSVS 7

RESULT 33
A46306
spasmogenic toxin PNVI - spider (Phoneutria nigriverter) (fragment)
C/Species: Phoneutria nigriverter
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
C/Accession: A46306
R/Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.
Toxicol. 31, 377-384, 1993
A/Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide
A/Reference number: A46306; MUID:93276438; PMID:8503129
A/Accession: A46306
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-8 <MAR>

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
: : :
Db 5 GQST 8

RESULT 34
A14683
aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragm
N/Alternate names: aspartate aminotransferase, mitochondrial
C/Species: Gallus gallus (chicken)
C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C/Accession: A14683
R/Wilson, K.V.; Hunziker, P.; Hughes, G.J.
FEBS Lett. 108, 98-102, 1979
A/Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.
A/Reference number: A14683; MUID:80092116; PMID:520566
A/Accession: A14683
A/Molecule type: protein
A/Residues: 1-8 <WIL>
C/Keywords: aminotransferase; mitochondrion

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
: : :
Db 5 GQPK 8

RESULT 35
PT0323
Ig heavy chain CVD3 region (clone J2-106B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0323
R/Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jo
A/Reference number: PT0222; MUID:9108337; PMID:1899102
A/Accession: PT0323
A/Molecule type: DNA
A/Residues: 1-8 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
: : :
Db 4 GQRR 7

RESULT 36
PN0043
phosphatidylethanol amine-binding protein - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C/Accession: PN0043
R/Kato, H.
Kawasaki Igakaishi 22, 245-259, 1996
A/Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neurot
A/Reference number: PN0041
A/Accession: PN0043
A/Molecule type: protein
A/Residues: 1-8 <KAT>
A/Experimental source: neuroblastoma cell
C/Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is blocked.
C/Keywords: brain

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4
: : :
Db 3 EQLS 6

RESULT 37
I49404
prealbumin - western wild mouse (fragment)
C/Species: Mus spretus (western wild mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C/Accession: I49404
R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A/Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A/Reference number: I48934; MUID:94319082; PMID:8043949
A/Accession: I49404
A/Status: preliminary; translated from GB/EMBL/DDBT
A/Molecule type: DNA
A/Residues: 1-8 <RES>
A/Cross-references: EMBL:U05689; NID:G497008; PIDN:AA60461.1; PID:G642825

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 20.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXH 7
:|:|:
Db 1 AVVSN 5

RESULT 38

C39690
neural cell adhesion molecule, cardiac splice form '-', '-' - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C/Accession: C39690
R/Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A/Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mR
A/Reference number: A39690; MUID:91141516; PMID:1596115
A/Accession: C39690
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A/Molecule type: mRNA
A/Residues: 1-8 <REY>
A/Cross-references: GB:M63970
C/Keywords: cardiac muscle; cell adhesion; heart

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 XQXX 4
:|:|:
Db 3 VQGE 6

RESULT 39

A35180
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C/Accession: A35180
R/Toshitaka, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.
J. Biol. Chem. 265, 5809-5815, 1990
A/Title: Purification of a novel type of calcium-activated neutral protease from rat bra
A/Reference number: A35180; MUID:90202830; PMID:2318836
A/Accession: A35180
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-8 <YOS>
C/Keywords: hydrolase

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 XQXXVX 6
:|:|:|:
Db 3 LSEGV 8

RESULT 40

S29272
tocopherol-binding protein, 81K - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C/Accession: S29272
R/Nalecz, K.A.; Nalecz, M.J.; Azzi, A.
Eur. J. Biochem. 209, 37-42, 1992
A/Title: Isolation of tocopherol-binding proteins from the cytosol of smooth muscle A7r5
A/Reference number: S29272; MUID:93011150; PMID:1396710
A/Accession: S29272
A/Molecule type: protein
A/Residues: 1-8 <NAL>
A/Experimental source: smooth muscle A7r5 cells

Query Match 32.0%; Score 8; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 XQXX 4
:|:|:
Db 4 DQXQ 7

RESULT 41

A61348
red pigment-concentrating hormone - northern shrimp
N/Alternate names: blanching hormone
C/Species: Pandalus borealis (northern shrimp)
C/Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C/Accession: A61348; S07139
R/Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A/Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A/Reference number: A61348; MUID:72228738; PMID:5041363
A/Accession: A61348
A/Molecule type: protein
A/Residues: 1-8 <FER1>

R/Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974

A/Title: Structure of the red pigment-concentrating hormone of the shrimp, Pandalus bore
A/Reference number: S07139; MUID:75054965; PMID:4433569
A/Accession: S07139

A/Molecule type: protein
A/Residues: 'E', 2-8 <FER2>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C/Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pic
zed pigment-containing cells.

C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/6/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.0%; Score 7; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QXX 4
:|:|:
Db 1 QLN 3

RESULT 42

A28004
adipokinetic hormone G - two-spotted cricket
N/Alternate names: AKH-G
C/Species: Gryllus bimaculatus (two-spotted cricket)
C/Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997
C/Accession: A28004
R/Gaede, G.; Rinehart, K.L.
Biochem. Biophys. Res. Commun. 149, 908-914, 1987
A/Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptic
A/Reference number: A28004; MUID:88106553; PMID:3426616
A/Accession: A28004
A/Molecule type: protein
A/Residues: 1-8 <GAB>
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/6/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.0%; Score 7; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QXX 4
:|:|:
Db 1 QVN 3

RESULT 43

S08995 hypertrehalosemic hormone I - oriental cockroach

N/Alternate names: Pea-CAH-I

C/Species: Blatta orientalis (oriental cockroach)

C/Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997

C/Accession: S08995

R/Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard

A/Reference number: S08995; PMID:90253659; PMID:2340112

A/Accession: S08995

A/Molecule type: protein

A/Residues: 1-8 <GAE>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.0%; Score 7; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QVN 3

RESULT 44

S08996 hypertrehalosemic hormone II - oriental cockroach

N/Alternate names: Pea-CAH-II

C/Species: Blatta orientalis (oriental cockroach)

C/Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997

C/Accession: S08996

R/Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard

A/Reference number: S08995; PMID:90253659; PMID:2340112

A/Accession: S08996

A/Molecule type: protein

A/Residues: 1-8 <GAE>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.0%; Score 7; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QVN 3

RESULT 45

S10596

adipokinetic hormone - pond skimmer

C/Species: Libellula auripennis

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997

C/Accession: S10596

R/Gaede, G.

Biol. Chem. Hoppe-Seyler 371, 475-483, 1990

A/Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating ho

A/Reference number: S10596; PMID:90359055; PMID:2390213

A/Accession: S10596

A/Molecule type: protein

A/Residues: 1-8 <BIO>

C/Comment: This peptide has both adipokinetic and hypertrehalosemic activities.

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.0%; Score 7; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QVN 3

Search completed: August 19, 2004, 15:51:22
Job time : 12.5 secs

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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 ; Search time 8 Seconds

(Without alignments)
52.070 Million cell updates/sec

Title: VARIANT1

Sequence: 1 XQXXVHL 8

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	48.0	8	1 FUSO_FUSO	P81010 fusarium so
2	11	44.0	8	1 ACI_THUL	P18691 thunnus alb
3	10	40.0	8	1 ANG2_BORJA	Q10582 bothrops ja
4	10	40.0	8	1 CPD1_ENTFA	P13269 enterococcu
5	10	40.0	8	1 UPAL_HUMAN	P20087 homo sapien
6	9	36.0	8	1 ALI1_CYPDO	P82152 cydia pomon
7	9	36.0	8	1 COXG_RAT	P80430 rattus norv
8	9	36.0	8	1 GLUR_HUMAN	P02729 homo sapien
9	9	36.0	8	1 LCK4_LEUMA	P21143 leucophaea
10	9	36.0	8	1 LCK6_LEUMA	P19988 leucophaea
11	8	32.0	8	1 ACT_CARMA	P80709 carcinus ma
12	8	32.0	8	1 ALI7_CARMA	P81820 carcinus ma
13	8	32.0	8	1 B44K_PORGI	P81886 porphyromon
14	8	32.0	8	1 CLP_THICU	P80488 thiochacilly
15	8	32.0	8	1 LCK3_LEUMA	P21142 leucophaea
16	8	32.0	8	1 NPM8_BOVIN	P15507 bos taurus
17	8	32.0	8	1 UC26_MAIZE	P80632 zea mays (m
18	8	32.0	8	1 UP06_MOUSE	P38644 mus musculu
19	8	32.0	8	1 UH09_RAT	P56575 rattus norv
20	7	28.0	8	1 AKHG_GRYBI	P41068 gryllus bim
21	7	28.0	8	1 AKH_LIBAU	P25418 libellula a
22	7	28.0	8	1 AKH_MEML	P25423 melolontha
23	7	28.0	8	1 AKH_TYBKT	P14595 tabanus atr
24	7	28.0	8	1 CAD1_ENTFA	P13268 enterococcu
25	7	28.0	8	1 COM2_CONPU	P8785 consus purpu
26	7	28.0	8	1 FAR4_MACRS	P83277 macrobrachi
27	7	28.0	8	1 HTP1_PBRAM	P45458 periplaneta
28	7	28.0	8	1 HTP2_PBRAM	P4549 periplaneta
29	7	28.0	8	1 HTP_TENNO	P25419 tenebrio mo
30	7	28.0	8	1 LMT2_LOCOMI	P22356 locusta mig
31	7	28.0	8	1 LPK_LEUMA	P13049 leucophaea
32	7	28.0	8	1 PLP_BRANA	P81707 brassica na
33	7	28.0	8	1 PPK2_PBRAM	P82692 periplaneta

34	7	28.0	8	1 RPCH_PANBO	P08939 pandanus bo
35	7	28.0	8	1 VGIG_HSV2B	P81780 herpes simp
36	6	24.0	8	1 ALI2_CARMA	P81815 carcinus ma
37	6	24.0	8	1 ALI7_CARMA	P81809 carcinus ma
38	6	24.0	8	1 FAR1_FENMO	P83316 penaeus mon
39	6	24.0	8	1 FAR2_MACRS	P83275 macrobrachi
40	6	24.0	8	1 FAR3_HOMAM	P41486 homarus ame
41	6	24.0	8	1 FAR4_HOMAM	P41487 homarus ame
42	6	24.0	8	1 FAR7_ASCSU	P43171 ascaris suu
43	6	24.0	8	1 NS3_MYCTU	P81152 mycobacteri
44	6	24.0	8	1 PPK3_PBRAM	P82618 periplaneta
45	6	24.0	8	1 RT34_BOVIN	P82929 bos taurus

ALIGNMENTS

RESULT 1
FUSO_FUSO STANDARD; PRT; 8 AA.
ID P81010;
AC P81010;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus s I3596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
ON NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RL Submitted (JUL-1997) to Swiss-Prot.
CC -!- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON TER
SQ SEQUENCE 8 AA; 898 MW; C372C41F5B69041 CRC64;

Query Match 48.0%; Score 12; DB 1; Length 8;
Best Local Similarity 20.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 XXVXH 7
Db 1 TIMSH 5

RESULT 2
ACI_THUL STANDARD; PRT; 8 AA.
ID P18691;
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
ON NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326332; PubMed=3415688;
RA Kohana Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna muscle."
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR; A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 44.0%; Score 11; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHL 8
 DB 2 TH1 4

RESULT 3

ANG2_BOTUA STANDARD; PRT; 8 AA.
 AC Q10582;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide II (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Bothrops.
 NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgneresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 plasma of the snake Bothrops jararaca."
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KM Vasconstrictor; Plasma; Serpin.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 40.0%; Score 10; DB 1; Length 8;
 Best Local Similarity 20.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
 DB 2 RYVH 6

RESULT 4

CPD1_ENTFA STANDARD; PRT; 8 AA.
 ID CPD1_ENTFA
 AC P13269;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CPD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Larva;
 RX MEDLINE=85040388; PubMed=6436978;
 RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B.;
 RT "Isolation and structure of bacterial sex pheromone, CPD1."
 RL Science 226:849-850(1984).
 CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC BACTERIOPHAGE PLASMID PPD1.
 KM Pheromone.
 SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 40.0%; Score 10; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 8
 DB 1 FLVWFL 6

RESULT 5

UPAL_HUMAN STANDARD; PRT; 8 AA.
 ID UPAL_HUMAN
 AC P30087;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tisot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing."
 RL Electrophoresis 13:707-714(1992).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 protein is: 4.9, its MW is: 65 kDa.
 DR SWISS-2DPAGE; P30087; HUMAN.
 FT NON_TER 1 1
 FT UNSURE 8 8
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 944 MW; C01772C45BB06DA CRC64;

Query Match 40.0%; Score 10; DB 1; Length 8;
 Best Local Similarity 16.7%; Pred. No. 1.4e+05;
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XOXVX 6
 DB 2 QESNP 7

RESULT 6

ALL1_CYPDO STANDARD; PRT; 8 AA.
 ID ALL1_CYPDO
 AC P82152;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 1.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dioryssa;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily."
 RL Peptides 16:1301-1309(1997).
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 KM Neuropeptide; Amidation.
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 36.0%; Score 9; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 XH 7
:|
Db 2 PH 3

RESULT 7

COXG_RAT STANDARD; PRT; 8 AA.
ID COXG_RAT
AC P80430;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIb (EC 1.9.3.1) (AED) (Fragment).
GN COX6B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RP SEQUENCE.
RC STRAIN=Mistar; TISSUE=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform."
RL Bur. J. Biochem. 230:235-241(1995).
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport. This protein may be one of the
CC heme-binding subunits of the oxidase.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase VIb family.
DR PIR; S65381; S65381.
KW Oxidoreductase; Mitochondrion.
FT NON TER 1
FT NON TER 8
FT NON TER 8
SQ SEQUENCE 8 AA; 1039 MW; 8101E9CAA73AE456 CRC64;
Query Match 36.0%; Score 9; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QXXVX 6
:|:
Db 1 QNXLD 5

RESULT 8

GLUR_HUMAN STANDARD; PRT; 8 AA.
ID GLUR_HUMAN
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urine glycopeptide.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar
RT glycopeptide containing cysteinyl-galactose."
RL Biochem. J. 123:25P-25P(1971).
CC -1- FUNCTION: The identity of the glycoprotein from which this peptide
CC is derived is unknown. No physiological function has been
CC attributed. An erythrocyte membrane glycopeptide having a
CC similar structure has also been found.
PIR; A03186; XGHUHU.

DR GO; GO:0005576; C:extracellular; NAS.
KM Glycoprotein.
FT CARBOHYD 1
SQ SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;

Query Match 36.0%; Score 9; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 XH 7
:|
Db 2 EH 3

RESULT 9

LCK6_LEUMA STANDARD; PRT; 8 AA.
ID LCK6_LEUMA
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT cephalomyotropic peptides."
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach proctodaeum (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
KW Neuropeptide; Amidation.
FT MOD_RES 8
FT MOD_RES 8
SQ SEQUENCE 8 AA; 906 MW; DC6365B1B95BDDA CRC64;
Query Match 36.0%; Score 9; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 6 XH 7
:|
Db 4 FH 5

RESULT 10

LCK6_LEUMA STANDARD; PRT; 8 AA.
ID LCK6_LEUMA
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile

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CC activity of cockroach prothorax (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; JS0316; JS0316.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 935 MW; 9D635B1B9D5A5A6 CRC64;

Query Match
Best Local Similarity 36.0%; Score 9; DB 1; Length 8;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 XH 7
Db 4 FH 5

RESULT 11
ACT_CARMA STANDARD; PRT; 8 AA.
ID ACT_CARMA STANDARD; PRT; 8 AA.
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin (Fragment).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA Bachassarian D.;
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL Endocrine 5:23-32(1996).
CC -1- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8. ITS MW IS: 46 kDa.
CC -1- SIMILARITY: Belongs to the actin family.
CC InterPro: IPR004001; Actin.
DR InterPro: IPR004000; Actin like.
DR PROSITE: PS00406; ACTINS_1; PARTIAL.
DR PROSITE: PS00432; ACTINS_2; PARTIAL.
DR PROSITE: PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAB3 CRC64;

Query Match
Best Local Similarity 32.0%; Score 8; DB 1; Length 8;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 OXVX 6
Db 1 KCDVD 5

RESULT 12
AL17_CARMA STANDARD; PRT; 8 AA.
ID AL17_CARMA STANDARD; PRT; 8 AA.
AC P81870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 17.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

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OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Jonhnen A.H., Maestro J.-L., Scott A.G., Jaroš P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 8 AMIDATION (POTENTIAL).
SQ SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;

Query Match
Best Local Similarity 32.0%; Score 8; DB 1; Length 8;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXX 4
Db 2 QOXS 5

RESULT 13
B44K_PORGI STANDARD; PRT; 8 AA.
ID B44K_PORGI STANDARD; PRT; 8 AA.
AC P818E6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 44 kDa immunogenic protein (Fragment).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE.
RC STRAIN=VJB 3492;
RX MEDLINE=20198497; PubMed=10731616;
RA Norris J.W., Love D.N.;
RT "Serum antibody responses of cats to soluble whole cell antigens of
RT feline Porphyromonas gingivalis.";
RL Vet. Microbiol. 73:37-49(2000).
CC -1- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
KW Antigen.
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match
Best Local Similarity 32.0%; Score 8; DB 1; Length 8;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXX 4
Db 3 YQKR 6

RESULT 14
CLP_THICU STANDARD; PRT; 8 AA.
ID CLP_THICU STANDARD; PRT; 8 AA.
AC P80488;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemolichotroph-specific protein (Fragment).
OS Thiodacillus cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Thiomonas.
OX NCBI_TaxID=36860;
RN [1]

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RP SEQUENCE.
 RC STRAIN=DSM 5494;
 RA Marin I., Amaro A.M., Jerez C.A., Amile R., Abad J.P.;
 RU Submitted (SSP-1995) to Swiss-Pat.
 CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
 CC CHEMOLITHOTROPHICALLY.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 785 MW; 91487806DDC2D76D CRC64;
 Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XXXX 4
 DB 4 ADEG 7

RESULT 15
 LCK3_LEUMA
 ID LCK3_LEUMA STANDARD; PRT; 8 AA.
 AC P2112;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leucokinin III (L-III).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxId=6988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Primary structure and synthesis of two additional neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT Cephalomyotropins.";
 RL Cephalomyotropins.";
 CC Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
 CC activity of cockroach proctodeum (hindgut).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 KM Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;
 Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XXXX 4
 DB 1 DQGF 4

RESULT 16
 NPMB_BOVIN
 ID NPMB_BOVIN STANDARD; PRT; 8 AA.
 AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Morphine modulating neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxId=9913;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RX MEDLINE=80667985; PubMed=1865193;
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;

RT "Isolation, sequencing, synthesis, and pharmacological
 RT characterization of two brain neuropeptides that modulate the action
 RT of morphine.";
 RU Proc. Natl. Acad. Sci. U.S.A. 82:757-776(1985).
 CC -1- FUNCTION: Modulates the action of morphine.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR; B24749; B24749.
 KM Neuropeptide; Amidation.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;
 Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XXXX 4
 DB 3 FOPQ 6

RESULT 17
 UC26_MAIZE
 ID UC26_MAIZE STANDARD; PRT; 8 AA.
 AC P80632;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
 DE (fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxId=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huot J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 7.0, its MW is: 57.2 kDa.
 DR Maize-2DPAGE; P80632; COLEOPTILE.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;
 Query Match 32.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XXXX 4
 DB 5 DQFK 8

RESULT 18
 UF06_MOUSE
 ID UF06_MOUSE STANDARD; PRT; 8 AA.
 AC P38644;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P50) (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;

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RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Paterson R.M., Michler L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994)
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.2, its MW is: 50 KDa.
FT NON TER 8
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 H 7
DB 1 H 1

RESULT 19
UH09 RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Mistar; TISSUE=Heart;
RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 8.9, its MW is: 42 KDa.
FT NON TER 8
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXX 4
DB 4 ROSP 7

RESULT 20
AKHG GRVBI STANDARD; PRT; 8 AA.
ID AKHG GRVBI
AC P14066;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_Taxid=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G. bimaculatus; TISSUE=Corpora cardiaca;
RA MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokinetic activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus.";
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RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R. microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -1- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4
DB 1 QVN 3

RESULT 21
AKH LIBAU STANDARD; PRT; 8 AA.
ID AKH LIBAU
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_Taxid=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -1- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4
DB 1 QVN 3
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Db 1 QVN 3

RESULT 22

AKH_MELML

AC P25423; STANDARD; PRT; 8 AA.

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adipokinetic hormone (AKH).

OS Melolontha melolontha (Cockchafer), and

OS Geotrupes stercorarius (Dor beetle), and

OS Pachnoda marginata (Flower beetle).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;

OC Scarabaeidae; Melolonthinae; Melolontha.

OX NCBI_TaxID=7061, 7087, 7058;

RN [1]

RP SEQUENCE.

RC SPECIES=M.melolontha, and G.stercorarius; TISSUE=Corpora cardiaca;

RX MEDLINE=91248100; Pubmed=2039445;

RA Gaede G.;

RT "A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species."

RL Biochem. J. 275:671-677 (1991).

RN [2]

RP SEQUENCE.

RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;

RX MEDLINE=92265187; Pubmed=1586453;

RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;

RT "Primary structures of neuropeptides isolated from the corpora cardiaca of various cetonid beetle species determined by pulsed-liquid phase sequencing and tandem fast atom bombardment mass spectrometry."

RT Biol. Chem. Hoppe-Seyler 373:133-142 (1992).

RL -1- FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight muscles to use these diglycerides as an energy source.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.

DR PIR: A56641; A58641.

DR PIR: S15422; S15422.

DR PIR: S21663; S21663.

DR InterPro: IPR002047; AKH.

DR PROSITE: PS00256; AKH; 1.

KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.

FT MOD_RES 1 8 AMIDATION: PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 1 8 AMIDATION: PYRROLIDONE CARBOXYLIC ACID.

FT SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

QY 2 QXX 4

Db 1 QLN 3

Query Match 28.0%; Score 7; DB 1; Length 8;

Best Local Similarity 33.3%; Pred. No. 1.4e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 23

AKH_TABAT

ID AKH_TABAT STANDARD; PRT; 8 AA.

AC P14595;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I) (DCC I).

OS Tabanus arctus (Horse fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;

OC Tabanus.

OX NCBI_TaxID=7207;

RN [1]

RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RX MEDLINE=90046758; Pubmed=2813385;

RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,

RA Vogel V.W., Zhang Y.-S., Hayes D.K.;

RT "Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activity isolated from the corpora cardiaca of horse flies (Diptera)."

RT Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).

RL -1- FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight muscles to use these diglycerides as an energy source.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.

DR PIR: A33995; A33995.

DR InterPro: IPR002047; AKH.

DR PROSITE: PS00256; AKH; 1.

KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.

FT MOD_RES 1 8 AMIDATION: PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 1 8 AMIDATION: PYRROLIDONE CARBOXYLIC ACID.

FT SEQUENCE 8 AA; 949 MW; 86786771A9DA1A736 CRC64;

QY 2 QXX 4

Db 1 QLT 3

Query Match 28.0%; Score 7; DB 1; Length 8;

Best Local Similarity 33.3%; Pred. No. 1.4e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 24

CAD1_ENTFA

ID CAD1_ENTFA STANDARD; PRT; 8 AA.

AC P13268;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-FEB-1991 (Rel. 17, Last annotation update)

DE Sex pheromone CAD1.

OS Enterococcus faecalis (Streptococcus faecalis).

OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI_TaxID=1351;

RN [1]

RP SEQUENCE.

RX MEDLINE=85051869; Pubmed=6437873;

RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,

RA Craig R.A., Clewell D.B., Suzuki A.;

RT "Isolation and structure of the bacterial sex pheromone, CAD1, that induces plasmid transfer in Streptococcus faecalis."

RL FEMS Lett. 178:97-100 (1994).

CC -1- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE

CC HEMOLYSIN PLASMID PAD1.

KW Pheromone.

FT SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

QY 3 XXVX 6

Db 3 SLVL 6

Query Match 28.0%; Score 7; DB 1; Length 8;

Best Local Similarity 25.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 25

COM2_CONPU

ID COM2_CONPU STANDARD; PRT; 8 AA.

AC P58785;

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leu-contryphan-P.
 OS Conus purpurascens (Purple cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxId=41690;
 (1)
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC STRAIN-Clipperton Island; TISSUE=Venom;
 RX MEDLINE=99388839; Pubmed=10461743;
 RA Jacobsen R.B.; Jimenez E.C.; De la Cruz R.G.C.; Gray W.R.; Cruz L.J.;
 RA Olivera B.M.;
 RT "A novel D-leucine-containing Conus peptide: diverse conformational
 dynamics in the contryphan family."
 RL J. Pept. Res. 54:93-99(1999).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
 CC -1- SIMILARITY: Belongs to the contryphan family.
 KM Toxin; Hydroxylation: D-amino acid.
 FT DISUFID 2 8
 FT MOD RES 4 4
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6
 : : :
 DB 1 GCVL 4

RESULT 26
 FAR4 MACRS STANDARD; PRT; 8 AA.
 ID FAR4 MACRS
 AC P83277;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLp4 (APALRLP-amide).
 OS Macrobrachium rosenbergii (Giant freshwater prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxId=79674;
 (1)
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RA Sitihongnui P.; Sarathongkum W.; Jaidechoev S.; Longyant S.;
 RA Sitihongnui W.;
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
 freshwater prawn Macrobrachium rosenbergii.";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -1- MASS SPECTROMETRY: MW=943; METHOD=WALDI.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.
 CC GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8
 FT AMIDATION.
 SQ SEQUENCE 8 AA; 943 MW; 9CD40734072DC76D CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 16.7%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 XXVXHL 8
 : : :
 DB 1 APALRL 6

RESULT 27
 HTFL PERAM STANDARD; PRT; 8 AA.
 ID HTFL PERAM
 AC P04548;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrihaloasemic factor I (Neuropeptide M-I) (Periplaneta CC-1)
 DE (Pea-CAH-1) (Led-CC-1) (Hypertrihaloasemic neuropeptide I).
 OS Periplaneta americana (American cockroach).
 OS Leptinocara decemlineata (Colorado potato beetle), and
 OS Blattella orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxId=6978, 7539, 6976;
 (1)
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=85046530; Pubmed=6548628;
 RA Wilten J.L.; Schaffer M.H.; O'Shea M.; Cook J.C.; Hemling M.E.;
 RA Rinehart K.L. Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 bombardment mass spectrometry."
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=84298179; Pubmed=6591205;
 RA Scarborough R.M.; Jamieson G.C.; Kalish F.; Kramer S.J.; McEnroe G.A.;
 RA Miller C.A.; Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; Pubmed=2576128;
 RA Gaede G.; Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical."
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; Pubmed=2340112;
 RA Gaede G.; Rinehart K.L. Jr.;
 RT "Primary structures of hypertrihaloasemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphodrhina portentosa, Blattella germanica and Blattella orientalis
 RT and of the stick insect Exaltoloma tilatrum assigned by tandem fast
 RT atom bombardment mass spectrometry."
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: Hypertrihaloasemic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph (trehalose is
 CC the major carbohydrate in the hemolymph of insects).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 CC PIR; A05169; A05169.
 DR PIR; A44960; A44960.
 DR PIR; A49823; A49823.
 DR PIR; S08995; S08995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 FT PYRROLIDONE CARBOXYLIC ACID.
 FT AMIDATION.
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4
|::
Db 1 QVN 3

RESULT 28
HTF2_PERAM STANDARD; PRT; 8 AA.

ID HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplaneta CC-2)
DE (P6A-CAH-II) (Led-CC-II) (Hypertrehalosaemic neuropeptide II).
OS Periplaneta americana (American cockroach).
OS Lepidocara decemlineata (Colorado potato beetle), and
OS Blattella orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattellidae; Periplaneta.
OC NCBI_TaxID=6978, 7539, 6976;
[1]
RN
RP SEQUENCE.
RC SPECIES=P. americana;
RX MEDLINE=85046530; Pubmed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry."
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
[2]
RN
RP SEQUENCE.
RC SPECIES=P. americana;
RX MEDLINE=84298179; Pubmed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana."
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
[3]
RN
RP SEQUENCE.
RC SPECIES=L. decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; Pubmed=2576128;
RA Gaede G., Rinehart K.L. Jr.;
RT "The metabolic neuropeptides of the corpora cardiaca from the potato
RT beetle and the American cockroach are identical."
RL Peptides 10:1287-1289(1989).
[4]
RN
RP SEQUENCE.
RC SPECIES=B. orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; Pubmed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blattella orientalis
RT and of the stick insect Exaltosoma tilarum assigned by tandem fast
RT atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
-1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08966; S08966.
DR INTERPRO; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KM Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A3D1A736 CRC64;
Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4
|::
Db 1 QVN 3

RESULT 29
HTF2_PERAM STANDARD; PRT; 8 AA.

ID HTF2_PERAM STANDARD; PRT; 8 AA.
AC P25419;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor (HOTH) (Hypertrehalosaemic neuropeptide).
OS Tenebrio molitor (Yellow mealworm), and
OS Zophobas rugipes.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OC NCBI_TaxID=7067, 7075;
[1]
RN
RP SEQUENCE.
RC SPECIES=T. molitor, and Z. rugipes;
RX TISSUE=Corpora cardiaca;
RX MEDLINE=90341081; Pubmed=2381871;
RA Gaede G., Rosinski G.;
RT "The primary structure of the hypertrehalosaemic neuropeptide from
RT tenebrionid beetles: a novel member of the AKH/RPCH family."
RL Peptides 11:455-459(1990).
-1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR PIR; A43976; A43976.
DR PIR; B43976; B43976.
DR INTERPRO; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KM Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;
Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4
|::
Db 1 QVN 3

RESULT 30
HTF2_LOCM1 STANDARD; PRT; 8 AA.

ID HTF2_LOCM1 STANDARD; PRT; 8 AA.
AC P22356;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Locustamyotropin 2 (LOM-MT-2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OC NCBI_TaxID=7004;
[1]
RN
RP SEQUENCE.

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RC TISSUE=Corpora cardiaca;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin II, an
RT additional neuropeptide of Locusta migratoria. Member of the
RT cephalomyotrophic peptide family.";
RL Insect Biochem. 20:479-484(1990).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotrophic
CC activity).
CC -1- SIMILARITY: Belongs to the pyrokinin family.
CC InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 AA; 934 MW; 26341771A9CA87B CRC64;
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 16.7%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 XXVXHL 8
Db 3 DFTPRL 8

RESULT 31
LPK_LEUMA STANDARD; PRT; 8 AA.
ID LPK_LEUMA
AC P13049;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leukopyrokinin (LPK) (LEW-PK).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OC NCBI_Taxid=6988;
OX (1)
RN
RP SEQUENCE.
RX MEDLINE=86269041; PubMed=3015140;
RA Nachman R.J., Holman G.M., Cook B.J.;
RT "Active fragments and analogs of the insect neuropeptide
RT leucopyrokinin: structure-function studies.";
RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
RN (2)
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of a blocked myotrophic
RT neuropeptide isolated from the cockroach, Leucophaea maderae.";
RL Comp. Biochem. Physiol. 85C:219-224(1986).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotrophic
CC activity).
CC -1- MISCELLANEOUS: An analog without the N-terminal PCA residue was
CC synthesized and found to exhibit greater activity (144% than the
CC parent neuropeptide. The portion of the sequence of LPK most
CC critical for the myotrophic properties is limited to the
CC pentapeptide fragment FTPLRL.
CC -1- SIMILARITY: Belongs to the pyrokinin family.
DR PIR: A23967; A23967.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

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Db 1 QTS 3

RESULT 32
PLP_BRANA STANDARD; PRT; 8 AA.
ID PLP_BRANA
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Placental lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_Taxid=3708;
RN (1)
RN SEQUENCE.
RC STRAIN=CV. TOPAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Rose J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus.";
RL Planta 208:588-598(1999).
CC -1- FUNCTION: May play a structural role in the elaioplast, a tapetum-
CC specific plastidial lipid organelle.
CC -1- TISSUE SPECIFICITY: Tapetum of anthers.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CA042 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVX 6
Db 2 IDVN 5

RESULT 33
PPK2_PERAM STANDARD; PRT; 8 AA.
ID PPK2_PERAM
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_Taxid=6978;
RN (1)
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotrophic
CC activity).
CC -1- TISSUE SPECIFICITY: Corpora cardiaca.
CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.

```

CC -1- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE: PS00539; PYROKININ. FALSE NEG.
 KM Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D77775 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 16.7%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 XXVXHL 8
 DB 3 PFAPRL 8

RESULT 34
 RPCH PANBO STANDARD; PRT; 8 AA.
 AC P08939;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Red pigment concentrating hormone (RPCH).
 OS Pandanus borealis (Northern red shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidae;
 OC Pandalidae; Pandalus.
 OX NCBI_TaxID=6703;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75054965; PubMed=4433569;
 RA Fernlund P.;
 RT "Structure of the red-pigment-concentrating hormone of the shrimp,
 Pandanus borealis.";
 RL Biochim. Biophys. Acta 371:304-311(1974).
 CC -1- FUNCTION: This hormone adapts the animal to light backgrounds by
 stimulating concentration of the pigment of its red body-
 chromophores.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH. 1;
 KM Pigment; Hormone; Amidation; Pyroliidone carboxylic acid.
 FT MOD RES 8 AMIDATION.
 FT MOD RES 1 PYROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QXX 4
 DB 1 QLN 3

RESULT 35
 VGLG HSV2B STANDARD; PRT; 8 AA.
 AC P81809;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Glycoprotein G (Fragment).
 OS Herpes simplex virus (type 2 / strain B4327UR).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=103921;
 RN [1]
 RP SEQUENCE.
 RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;

RL Submitted (APR-1999) to Swiss-Prot.
 CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
 CC 2: GH, GB, GC, GD, GI, AND GE.
 CC -1- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
 CC HSV-1.
 KM Glycoprotein.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6
 DB 2 SGVP 5

RESULT 36
 AL12 CARMA STANDARD; PRT; 8 AA.
 AC P81815;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinus maenas 12.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -1- SIMILARITY: Belongs to the allostatin family.
 KM Neuropeptide; Multigene family.
 SQ SEQUENCE 8 AA; 913 MW; 672879CDBC569AB7 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 12.5%; Pred. No. 1.4e+05;
 Matches 1; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 XQXXVXHL 8
 DB 1 PDMYAFGL 8

RESULT 37
 ALL7 CARMA STANDARD; PRT; 8 AA.
 AC P81809; P81804; P81810;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Carcinus maenas 7 [Contains: Carcinustatin 6; Carcinustatin 1].
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;

RT "Isolation and identification of multiple neuropeptides of the
 RL allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RC Bur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Amidation; Multigene family.
 FT PEPTIDE 1 8 CARCINOSTATIN 7.
 FT PEPTIDE 2 8 CARCINOSTATIN 6.
 FT PEPTIDE 4 8 CARCINOSTATIN 1.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 825 MW; 922879CDB475BD CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 12.5%; Pred. No. 1.4e+05;
 Matches 1; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 XQXXVXL 8
 DB 1 ASPIYAFGL 8

RESULT 38
 FARI_PENMO STANDARD; PRT; 8 AA.
 AC P83316;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLPI (GDRNFLRF-amide).
 OS *Peneaus monodon* (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Peneaus.
 OC NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigornngul P., Pupuem J., Krungkasem C., Longyant S.,
 RA Chaiyavithangkura P., Sithigornngul W., Petsom A.;
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 RT of the giant tiger prawn *Peneaus monodon*.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR GO:0007218; P-neuropeptide signaling pathway; TMS.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 DB 2 DRRNFLR 7

RESULT 39
 FAR2_MACRS STANDARD; PRT; 8 AA.
 AC P83275;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLPI2 (ADKXNFLRF-amide).
 OS *Macrobrachium rosenbergii* (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.

OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RA Sithigornngul P., Sarathongkum W., Jaidechoey S., Longyant S.,
 RA Sithigornngul W.;
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
 RT freshwater prawn *Macrobrachium rosenbergii*.";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -1- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR GO:0007218; P-neuropeptide signaling pathway; TMS.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C443AAD CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 DB 2 DRRNFLR 7

RESULT 40
 FAR3_HOMAM STANDARD; PRT; 8 AA.
 AC P414E6;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide 3 (FLI 3) (F2).
 OS *Homarus americanus* (American lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Nephropoidea; Nephropidae; Homarus.
 OC NCBI_TaxID=6706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=88116164; PubMed=3429714;
 RA Trimmer B.A., Koblitzki L.A., Kravitz E.A.;
 RT "Purification and characterization of FMRFamide-like immunoreactive
 RT substances from the lobster nervous system: isolation and sequence
 RT analysis of two closely related peptides.";
 RL J. Comp. Neurol. 266:16-26(1987).
 CC -1- MISCELLANEOUS: Pericardial organs release this peptide with 100 nm
 CC potassium in the presence of calcium.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 KW Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
 DB 2 DRRNFLR 7

RESULT 41
 FAR4_HOMAM STANDARD; PRT; 8 AA.
 AC P41487;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide 4 (FLI 4) (F1).

OS Homarus americanus (American lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Nephropidae; Nephropidae; Homarus.
 OX NCBI_TaxID=6706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=88116164; PubMed=3429714;
 RA Trimmer B.A., Kobler E.A., Kravitz E.A.;
 RT "Purification and characterization of FMRFamide-like immunoreactive
 substances from the lobster nervous system: isolation and sequence
 analysis of two closely related peptides.";
 RL J. Comp. Neurol. 266:16-26 (1987).
 CC -1- FUNCTION: Can act as a modulator of exoskeletal and cardiac
 neuromuscular junctions.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.
 CC Neuropeptide; Amidation.
 KM MOD RES 8
 FT SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;
 SQ
 Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XXXXX 6
 DB 2 NRNFLR 7
 RESULT 42
 FARP7_ASCSU STANDARD; PRT; 8 AA.
 ID FARP7_ASCSU
 AC P43171;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFamide-like neuropeptide AF7.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95380362; PubMed=7651904;
 RA Cowden C., Stretton A.O.W.;
 RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
 Ascaris suum.";
 RL Peptides 16:491-500 (1995).
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.
 CC Neuropeptide; Amidation.
 KM MOD RES 8
 FT SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;
 SQ
 Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 XXXX 6
 DB 4 RFR 7
 RESULT 43
 NS3_MYCTU STANDARD; PRT; 8 AA.
 ID NS3_MYCTU
 AC P81152;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30 kDa non-secretory protein 3 (Fragment).

OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=H37Rv;
 RA Prasad H.K., Annappurna P.S.;
 RL Submitted (DEC-1997) to Swiss-Prot.
 CC -1- CAUTION: We are unable to find this protein in the translation of
 the genome of strain H37Rv.
 CC FT NON TER 1 1
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 919 MW; 8D3DC40B19CDC2D2 CRC64;
 Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VXX 6
 DB 1 VVA 3
 RESULT 44
 PPK3_PERAM STANDARD; PRT; 8 AA.
 ID PPK3_PERAM
 AC P82618;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (PYPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144 (1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "A gamma-specific distribution of PXPRLamides in the nervous system of
 the American cockroach.";
 RL J. Comp. Neurol. 419:352-363 (2000).
 CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 activity).
 CC -1- TISSUE SPECIFICITY: Corpora cardiaca.
 CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MLDI.
 CC -1- SIMILARITY: Belongs to the pyrokinin family.
 KM MOD RES 8
 FT SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;
 SQ
 Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VXX 6
 DB 1 LVP 3
 RESULT 45
 RT34_BOVIN STANDARD; PRT; 8 AA.
 ID RT34_BOVIN

AC P82929;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).
 GN MRP834.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=21276436; PubMed=11279123;
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
 RT "The small subunit of the mammalian mitochondrial ribosome:
 RT identification of the full complement of ribosomal proteins present.";
 RL J. Biol. Chem. 276:19363-19374(2001).
 CC -1- SUBUNIT: Component of the mitochondrial ribosome small subunit
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1 8
 FT NON_TER 1 8
 SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6
 : : : :
 DB 2 WGITL 5

Search completed: August 19, 2004, 15:51:48
 Job time : 8 secs

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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 ; Search time 31 Seconds
(without alignments)
81.424 Million cell updates/sec

Title: VARIANT1

Perfect score: 25

Sequence: 1 XQXVXHL 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 414

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	15	60.0	8	4	Q7Z6G0
2	14	56.0	8	13	Q91098
3	14	56.0	8	13	Q90498
4	13	52.0	8	2	P72279
5	13	52.0	8	4	Q9UMC7
6	13	52.0	8	6	Q9XSY1
7	13	52.0	8	8	Q8WGC9
8	12	48.0	8	2	Q9ZEX9
9	12	48.0	8	2	O56246
10	12	48.0	8	2	Q8G940
11	12	48.0	8	2	P83152
12	12	48.0	8	5	Q9TWH6
13	12	48.0	8	9	Q34909
14	12	48.0	8	9	Q37854
15	12	48.0	8	13	P87488
16	12	48.0	8	13	P82082

17	11	44.0	8	4	Q15894	Q15894 homo sapien
18	11	44.0	8	4	Q9UDZ4	Q9UDZ4 homo sapien
19	11	44.0	8	5	Q9UMH9	Q9UMH9 homo sapien
20	11	44.0	8	5	O15899	O15899 babesia ovi
21	11	44.0	8	13	P79940	P79940 xenopus lae
22	11	44.0	8	13	P82083	P82083 limnodynast
23	10	40.0	8	2	Q45615	Q45615 bacillus eu
24	10	40.0	8	2	P77556	P77556 escherichia
25	10	40.0	8	2	Q93SP2	Q93SP2 pseudomonas
26	10	40.0	8	2	O8G121	O8G121 borrelia bu
27	10	40.0	8	3	O13591	O13591 saccharomyc
28	10	40.0	8	4	Q9BRT5	Q9BRT5 homo sapien
29	10	40.0	8	4	O15893	O15893 homo sapien
30	10	40.0	8	4	O8IUB8	O8IUB8 homo sapien
31	10	40.0	8	5	O8MUN6	O8MUN6 heliconius
32	10	40.0	8	5	O02032	O02032 lytechinus
33	10	40.0	8	5	O06BS9	O06BS9 strongyloce
34	10	40.0	8	6	Q9T778	Q9T778 canis fami
35	10	40.0	8	6	Q9BFR2	Q9BFR2 ursus arcto
36	10	40.0	8	6	Q9BFR2	Q9BFR2 macropus eu
37	10	40.0	8	6	Q9BFR9	Q9BFR9 tragalaphus
38	10	40.0	8	6	Q9BFR1	Q9BFR1 echinops te
39	10	40.0	8	6	Q9BFR1	Q9BFR1 ateltes fusc
40	10	40.0	8	6	Q9BFR7	Q9BFR7 capitis ind
41	10	40.0	8	6	Q9BFR9	Q9BFR9 euphractus
42	10	40.0	8	6	Q9BFR8	Q9BFR8 chaetophrac
43	10	40.0	8	6	Q9BFR0	Q9BFR0 macaca mula
44	10	40.0	8	6	Q9BFR8	Q9BFR8 loxodonta a
45	10	40.0	8	6	Q9BFR9	Q9BFR9 procavia ca

ALIGNMENTS

RESULT 1
ID Q7Z6G0 PRELIMINARY; PRT; 8 AA.
AC Q7Z6G0;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Fumarate hydratase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei M.-H., Nickerson M.L., Toro J.R.;
RT "dinucleotide repeat polymorphisms in the fumarate hydratase gene of
human chromosome 1q42.3.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY299638; AAF57532.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 881 MW; 40CSBIE732C4330 CRC64;

Query Match 60.0%; Score 15; DB 4; Length 8;
Best Local Similarity 40.0%; Pred. No. 1e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 XQXVXHL 7
Db 2 KNYVLAH 6

RESULT 2

ID Q91098 PRELIMINARY; PRT; 8 AA.
AC Q91098;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)

DE Myoglobin (Fragment).
 OS Manorina melanocephala (Noisy miner).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Meliphagidae; Manorina.
 NCBI_TaxID=44314;
 RX MEDLINE=95255652; PubMed=7737502;
 RP SEQUENCE FROM N.A.
 RC STRAIN=D02;
 RA Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;
 RT "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae
 assessed by temperature gradient gel electrophoresis.";
 RL Electrophoresis 19:142-151(1998).
 DR EMBL; U40497; AAC60364.1; -.
 FT NON_TER 1 8
 SQ SEQUENCE 8 AA; 890 MW; C6C1F2C865B046DE CRC64;

Query Match 56.0%; Score 14; DB 13; Length 8;
 Best Local Similarity 28.6%; Pred. No. 1e+06;
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XXXXXVH 7
 :|:::|
 DB 1 CQISGVH 7

RESULT 3
 Q90498 PRELIMINARY; PRT; 8 AA.
 AC Q90498;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
 DE Myoglobin (Fragment).
 OS Erythrura gouldiae (Gouldian finch).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Passeridae;
 OC Erythrura.
 NCBI_TaxID=44316;
 RX MEDLINE=95482272; PubMed=95482272;
 RC STRAIN=EGG1;
 RA Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;
 RT "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae
 assessed by temperature gradient gel electrophoresis.";
 RL Electrophoresis 19:142-151(1998).
 DR EMBL; U40496; AAC60363.1; -.
 FT NON_TER 1 8
 FT NON_TER 1 8
 SQ SEQUENCE 8 AA; 890 MW; C6C1F2C865B046DE CRC64;

Query Match 56.0%; Score 14; DB 13; Length 8;
 Best Local Similarity 28.6%; Pred. No. 1e+06;
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XXXXXVH 7
 :|:::|
 DB 1 CQISGVH 7

RESULT 4
 P72279 PRELIMINARY; PRT; 8 AA.
 AC P72279;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Biphenyl dioxygenase (Fragment).
 GN BPHB.
 OS Rhodococcus globerulus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.
 NCBI_TaxID=33008;
 RX MEDLINE=95255652; PubMed=7737502;
 RP SEQUENCE FROM N.A.
 RA Asturias J.A., Diaz B., Timmis K.N.;
 RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-
 positive bacterium Rhodococcus globerulus p6 to multicomponent
 dioxygenases of gram-negative bacteria.";
 RL Gene 156:11-18(1995).
 DR EMBL; X80041; CAA56350.1; -.
 DR GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
 KW Dioxygenase.
 FT NON_TER 1 8
 SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;

Query Match 52.0%; Score 13; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXVX 6
 :|:::|
 DB 3 LODERV 8

RESULT 5
 Q9UMC7 PRELIMINARY; PRT; 8 AA.
 AC Q9UMC7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE SHMT protein (Fragment).
 GN SHMT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=95482272; PubMed=95482272;
 RC STRAIN=EGG1;
 RA Chave K.J., Snell K., Sanders P.G.;
 RT "Isolation and characterisation of human genomic sequences encoding
 cytosolic serine hydroxymethyltransferase.";
 RL Biochem. Soc. Trans. 25:53-53(1997).
 DR EMBL; Y1492; CAB54844.1; -.
 FT NON_TER 1 8
 FT NON_TER 1 8
 SQ SEQUENCE 8 AA; 868 MW; 7C205721B44AB5B8 CRC64;

Query Match 52.0%; Score 13; DB 4; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHL 8
 :|:::|
 DB 4 NHL 6

RESULT 6
 Q9XSY1 PRELIMINARY; PRT; 8 AA.
 AC Q9XSY1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE Retinoblastoma protein (Fragment).
 GN RBL.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RX MEDLINE=9615;
 RP SEQUENCE FROM N.A.

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RX MEDLINE=97049323; PubMed=8894053;
RA Venter P.J., Brocchieri J.A., Yuzbasiyan-Gurkan V., Brewer G.J.;
RT "Gene-specific universal mammalian sequence-tagged sites: application
to the canine genome.";
RL Biochem. Genet. 34:321-341(1996).
RN [1]
RP SEQUENCE FROM N.A.
RA Venter P.J., Cao Y., Alexander L., Yuzbasiyan-Gurkan V.;
RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (Rb1)
gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF155737; AAD38807.1; -.
FT NON TER 1 1
SQ SEQUENCE 8 AA; 895 MW; 1425B18676721E3 CRC64;

Query Match 52.0%; Score 13; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHL 8
DB 1 KHL 3

RESULT 7
O8WGC9 PRELIMINARY; PRT; 8 AA.
ID O8WGC9;
AC O8WGC9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
OS Upogebia affinis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Thalassinidea;
OC Callinassoidae; Upogebidae; Upogebia.
OC NCBI_TaxID=177247;
RN [1]
RP SEQUENCE FROM N.A.
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
RA Cunningham C.W.;
RT "Mitochondrial gene rearrangements support a hypothesis of parallel
evolution to the crab-like form.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF436047; AAL31621.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 978 MW; FE20573B5452C056 CRC64;

Query Match 52.0%; Score 13; DB 8; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 1 MIVNYL 6

RESULT 8
O9ZEZ9 PRELIMINARY; PRT; 8 AA.
ID O9ZEZ9;
AC O9ZEZ9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
OS LeuA.
OS Buchnera aphidicola.
OC Plasmid pBRc1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

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OC Enterobacteriaceae; Buchnera.
RN NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99028904; PubMed=9812361;
RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
RT "Structure and evolution of the leucine plasmids carried by the
RT endosymbiont (Buchnera aphidicola) from aphids of the family
RT Aphididae.";
RL FEMS Microbiol. Lett. 168:43-49(1998).
DR EMBL; AJ006874; CAA07290.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0003852; F:2-isopropylmalate synthase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase; Plasmid.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 917 MW; FE205042D6C5B446 CRC64;

Query Match 48.0%; Score 12; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
DB 3 SQVITL 8

RESULT 9
O56246 PRELIMINARY; PRT; 8 AA.
ID O56246;
AC O56246; Q52410;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 05, Last sequence update)
DT 01-JAN-1998 (TREMBlrel. 08, Last annotation update)
DE Thermophilic proton ATPase epsilon subunit amino terminal (Fragment).
OS Thermophilic bacterium P53.
OC Bacteria; Firmicutes; Bacillales.
OC NCBI_TaxID=2334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PS3;
RX MEDLINE=87137359; PubMed=2880841;
RA Kagawa Y., Ishizuka M., Saitoh T., Nakao S.;
RT "Stable structure of thermophilic proton ATPase beta subunit.";
RL J. Biochem. 100:923-934(1986).
DR EMBL; D00113; BAA00067.1; -.
DR EMBL; X04609; CAA28278.1; -.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 914 MW; EBD5A2C1B041A336 CRC64;

Query Match 48.0%; Score 12; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 1 MKTIV 6

RESULT 10
O8G940 PRELIMINARY; PRT; 8 AA.
ID O8G940;
AC O8G940;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OS Bacterial group cp32-9, and plasmid group cp32-12.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]

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RP SEQUENCE FROM N.A.
 RC STRAIN=DN127c19-2, and Sh-2-82;
 RC PLASMID=group cp32-9, and group cp32-12;
 RA Stevenson B., Miller J.C.;
 RT "Comparative analyses of *Borrelia burgdorferi* erp genes and their cp32
 RT prophages: conservation amidst diversity.";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY142104; AN17853.1; -;
 DR EMBL; AY142097; AN17907.1; -;
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER
 SQ SEQUENCE 8 AA; 1042 MW; 1437244330504373 CRC64;
 Query Match 48.0%; Score 12; DB 2; Length 8;
 Best Local Similarity 14.3%; Pred. No. 1e+06;
 Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHL 8
 DB 1 KWIIXNL 7

RESULT 11
 ID P83152 PRELIMINARY; PRT; 8 AA.
 AC P83152;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Allophycocyanin beta chain (Fragment).
 OS Anabaena sp. (Strain L31).
 OC NCB1_TaxID=29412;
 RN [1]
 RP SEQUENCE.
 RA Apté S.K., Uhlemann E., Schmid R., Altendorf K.;
 RL Submitted (OCT-2001) to Swiss-Prot.
 CC -1- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
 CC FROM THE PHYCOBILIPROTEIN COMPLEX. ALLOPHYCOCYANIN HAS A MAXIMUM
 CC ABSORPTION AT APPROXIMATELY 650 TO 653 NANOMETERS.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.
 CC -1- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0030089; C:phycobillosome; IEA.
 DR GO; GO:0009579; C:thylakoid; IEA.
 DR GO; GO:0006119; P:electron transport; IEA.
 DR GO; GO:0015979; P:photosynthesis; IEA.
 KW Phycobillosome; Electron transport; Photosynthesis; Bile pigment;
 KW Thylakoid; Membrane.
 FT NON_TER
 SQ SEQUENCE 8 AA; 788 MW; 87CD0C1A05DDAB6DD CRC64;
 Query Match 48.0%; Score 12; DB 2; Length 8;
 Best Local Similarity 16.7%; Pred. No. 1e+06;
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XOXVX 6
 DB 1 AODAIT 6

RESULT 12
 ID Q9TWH6 PRELIMINARY; PRT; 8 AA.
 AC Q9TWH6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE BIOACTIVE peptide P4=PUTATIVE ESOPHAGEAL NEUROREGULATOR.
 OS *Perinereis vancaurica*.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;

OC Phyllodoceidae; Nereididae; Perinereis.
 OX NCB1_TaxID=6355;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95323338; PubMed=7599979;
 RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,
 RA Fujita T., Minakata H., Nomoto K.;
 RT "Isolation and characterization of four novel bioactive peptides from
 RT a polychaete annelid, *Perinereis vancaurica*."
 RL Comp. Biochem. Physiol. C, Pharmacol. Toxicol. Endocrinol. 110:297-
 RL 304(1995).
 SQ SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;
 Query Match 48.0%; Score 12; DB 5; Length 8;
 Best Local Similarity 14.3%; Pred. No. 1e+06;
 Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XOXVX 7
 DB 2 YEGDVY 8

RESULT 13
 ID Q34909 PRELIMINARY; PRT; 8 AA.
 AC Q34909;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Cytochrome b (Fragment).
 OS *Locusta migratoria* (Migratory locust).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCB1_TaxID=7004;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=88223478; PubMed=2836084;
 RX McCracken A., Uhlenbusch I., Gellissen G.;
 RT "Structure of the cloned locusta migratoria mitochondrial genome:
 RT restriction mapping and sequence of its ND-1 (URR-1) gene.";
 RL Curr. Genet. 11:625-630(1987).
 DR EMBL; X05286; CAA28905.1; -;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;
 Query Match 48.0%; Score 12; DB 8; Length 8;
 Best Local Similarity 20.0%; Pred. No. 1e+06;
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVX 7
 DB 4 IXLKH 8

RESULT 14
 ID Q37854 PRELIMINARY; PRT; 8 AA.
 AC Q37854;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Coliphage gene of unknown function, 5' end (Fragment).
 OS Bacteriophage R17.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Levivirus.
 OX NCB1_TaxID=12026;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=73224987; PubMed=4352721;
 RA Rensing U.F.E.;
 RT "A sequence of seventy-three nucleotides from the Colipage R17
 genome."
 RL Biochem. J. 131:593-604(1973).
 DR EMBL; M24820; AAA72755.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 969 MW; ECB45412C1E72726 CRC64;
 Query Match 48.0%; Score 12; DB 9; Length 8;
 Best Local Similarity 20.0%; Pred. No. 1e+06;
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 4 XXVXL 8
 DB 1 MLDLV 5
 RESULT 15
 ID P87488 PRELIMINARY; PRT; 8 AA.
 AC P87488;
 DT 01-MAY-1997 (TEMBLrel. 03, Created)
 DT 01-MAY-1997 (TEMBLrel. 03, Last sequence update)
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
 DE Growth hormone 2 (Fragment).
 GN GH-2-A OR GH-2-B.
 OS Oncorhynchus kisutch (Coho salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Procranchiopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 NX NCBI_TaxID=8019;
 RN [1]
 RP SEQUENCE OF 41-48 FROM N.A.
 RX MEDLINE=94173883; PubMed=8127856;
 RA Forbes S.H.; Knudsen K.L.; North T.W.; Allendorf F.W.;
 RT "One of two growth hormone genes in coho salmon is sex-linked."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:1628-1631(1994).
 DR EMBL; U04930; AAD13472.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 902 MW; 92233732D5A5B326 CRC64;
 Query Match 48.0%; Score 12; DB 13; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1e+06;
 Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 1 XQXXVXL 8
 DB 1 QKSSVLKL 8
 RESULT 16
 ID P82082 PRELIMINARY; PRT; 8 AA.
 AC P82082;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
 DE DYNASTIN 4.
 OS Limnodynastes salmuni (Salmun's-striped frog).
 OC Amphibia; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Limnodynastinae; Limnodynastes.
 NX NCBI_TaxID=39404;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RT TISSUE=SKIN SECRETION;

RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structure of the dynastins from
 RT Limnodynastes salmuni and Fletcherin from Limnodynastes fletcheri."
 RL Aust. J. Chem. 46:1235-1244(1993).
 CC -1- MASS SPECTROMETRY; MW=772; METHOD=FAE.
 SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;
 Query Match 48.0%; Score 12; DB 13; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 XXVXL 8
 DB 1 GLVSNL 6
 RESULT 17
 ID Q15894 PRELIMINARY; PRT; 8 AA.
 AC Q15894;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE (Clone XP587B) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta.
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Caskey C.T.H.; Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries."
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL; L32074; AAA73884.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 952 MW; BEC735B1E1F1B6D6 CRC64;
 Query Match 44.0%; Score 11; DB 4; Length 8;
 Best Local Similarity 20.0%; Pred. No. 1e+06;
 Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 XXVXH 7
 DB 1 MOTHN 5
 RESULT 18
 ID Q9UD24 PRELIMINARY; PRT; 8 AA.
 AC Q9UD24;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE RHD protein (Fragment).
 GN RHD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=97260406; PubMed=9106526;
 RA Matsui G., Cherif-Zahar B., Mouru I., Cartton J.P.;
 RT "Characterization of the recombination hot spot involved in the
 RT genomic rearrangement leading to the hybrid D-Ce-D gene in the DVI
 phenotype."
 RL Am. J. Hum. Genet. 60:808-817(1997).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=93066356; PubMed=1438298;
 RA Le Van Kim C., Mouru I., Cherif-Zahar B., Raynal V., Cherrier C.,
 RT "Molecular cloning and primary structure of the human blood group Rh
 polyepitope."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929(1992).
 DR EMBL; Z97031; CAB09727.1; -.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 1042 MW; D296944691FBSAB1 CRC64;
 Query Match 44.0%; Score 11; DB 4; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHL 8
 Db 3 YHM 5
 RESULT 19
 Q9UMH9 PRELIMINARY; PRT; 8 AA.
 ID Q9UMH9
 AC Q9UMH9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
 DE RHCE protein (Fragment).
 GN RHCE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=97260406; PubMed=9106526;
 RA Matsasi G., Cherif-Zahar B., Mouru I., Carttron J.P.,
 RT "Characterization of the recombination hot spot involved in the
 genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
 phenotype."
 RL Am. J. Hum. Genet. 60:808-817(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=90349591; PubMed=1696722;
 RA Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P.,
 RT "Molecular cloning and protein structure of a human blood group Rh
 polypeptide."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6243-6247(1990).
 DR EMBL; Z97030; CAB09726.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 1049 MW; C007244691FBSAB1 CRC64;
 Query Match 44.0%; Score 11; DB 4; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHL 8
 Db 3 YHM 5
 RESULT 20
 O15899 PRELIMINARY; PRT; 8 AA.
 AC O15899;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 12D3 antigen (Fragment).
 GN B012D3.
 OS Babesia ovis.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
 OX NCBI_TaxID=5869;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ankara;
 RA Silins G.U., Blakeley R.L., Riddles P.W.;
 RT "Characterization of the transcriptional control region of the 12D3
 antigen gene from the sporozoan Babesia ovis."
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBD databases.
 DR EMBL; U44919; AAB6365.1; -.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 992 MW; F0C7273411B2C726 CRC64;
 Query Match 44.0%; Score 11; DB 5; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 8
 Db 1 MLVTRL 6
 RESULT 21
 P79940 PRELIMINARY; PRT; 8 AA.
 ID P79940
 AC P79940;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE XMeisl-4 protein (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OX Xenopodinae; Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97202105; PubMed=9049632;
 RX Steelman S., Moskow J.J., Muzynski K., North C., Druck T.,
 RA Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.;
 RT "Identification of a conserved family of Meisl-related homeobox
 genes."
 RL Genome Res. 7:142-156(1997).
 DR EMBL; U68389; AAB19199.1; -.
 FT TRANSFAC; T03410; -.
 SQ SEQUENCE 8 AA; 1187 MW; 278B51F37B1F40B CRC64;
 Query Match 44.0%; Score 11; DB 13; Length 8;
 Best Local Similarity 16.7%; Pred. No. 1e+06;
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 OXXVXH 7
 Db 1 ERHEWH 6
 RESULT 22
 P82083 PRELIMINARY; PRT; 8 AA.
 ID P82083
 AC P82083;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE DYNASTIN 5.
 OS Limnodynastes salmiani (Salmian's-a-striped frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
OX NCBI_TaxID=39404;
RN (1)
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT Limnodynastes salmiani and Fletcherin from Limnodynastes fletcheri.";
RL Aust. J. Chem. 46:1235-1244(1993).
CC -1- MASS SPECTROMETRY: MW=786; METHOD=FAE.
SQ SEQUENCE 8 AA; 786 MW; 7858772455B05728 CRC64;

Query Match 44.0%; Score 11; DB 13; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 1 GLISNL 6

RESULT 23
ID Q45615 PRELIMINARY; PRT; 8 AA.
AC Q45615;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GucB protein (Fragment).
GN GUTB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94253000; PubMed=8195086;
RA Ye R., Wong S.L.;
RT "Transcriptional regulation of the Bacillus subtilis glucitol
RT dehydrogenase gene.";
RL J. Bacteriol. 176:3314-3320(1994).
DR EMBL; L16626; AAA20875.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXH 7
DB 1 MTH 3

RESULT 24
ID P77556 PRELIMINARY; PRT; 8 AA.
AC P77556;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE TRAY (Fragment).
GN TRAY.
OS Escherichia coli.
OC Plasmid incFII R1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ECOR11;
RX MEDLINE=96400908; PubMed=8807284;

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RA Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.;
RT "Mosaic structure of plasmids from natural populations of Escherichia
RT coli.";
RL Genetics 143:1091-1100(1996).
DR EMBL; U50661; AAC44245.1; -.
DR EMBL; U50650; AAC44234.1; -.
DR EMBL; U50651; AAC44235.1; -.
DR EMBL; U50652; AAC44236.1; -.
DR EMBL; U50653; AAC44237.1; -.
DR EMBL; U50654; AAC44238.1; -.
DR EMBL; U50655; AAC44239.1; -.
DR EMBL; U50656; AAC44240.1; -.
DR EMBL; U50657; AAC44241.1; -.
DR EMBL; U50658; AAC44242.1; -.
DR EMBL; U50659; AAC44243.1; -.
DR EMBL; U50660; AAC44244.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON TER 1
SQ SEQUENCE 8 AA; 834 MW; D35A5B0544735A1 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;
Best Local Similarity 12.5%; Pred. No. 1e+06;
Matches 1; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 XOXVXHL 8
DB 1 TSINISL 8

RESULT 25
ID Q93SP2 PRELIMINARY; PRT; 8 AA.
AC Q93SP2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Quaternary ammonium compound-resistance protein Qacdelta1
DE (Fragment).
GN QACBDELTH1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=YMC704; TRANSPOSON=class I integron;
RA Lee K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
RT "YIM-2 metallo-beta-lactamase gene-containing integron in a
RT Pseudomonas aeruginosa clinical isolate.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029772; AKK50441.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 920 MW; FE2729C732C87336 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 2 KGVLF 7

RESULT 26
ID Q8GL21 PRELIMINARY; PRT; 8 AA.
AC Q8GL21;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.

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OS Borrelia burgdorferi (Lyme disease spirochete).
OC Plasmid group cp32-8.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SH-2-82;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi exp genes and their cp32
  propargases: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142094; AAN17903.1; -.
GO GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON TER
SQ SEQUENCE 8 AA; 1042 MW; 1437244337204373 CRC64;

Query Match          40.0%; Score 10; DB 2; Length 8;
Best Local Similarity 14.3%; Pred. No. 1e+06;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 XXXVXH 8
DB 1 KWILKNL 7

RESULT 27
ID 01591 PRELIMINARY; PRT; 8 AA.
AC 01591;
DT 01-JUN-1998 (TREMBlrel. 05, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE ORF YNL337W (Fragment).
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycace.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermaier B., Piravandi E., Rinke M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z71612; CA96271.2; -.
FT NON TER
SQ SEQUENCE 8 AA; 1005 MW; 5CA441E449C9C720 CRC64;

Query Match          40.0%; Score 10; DB 3; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXXVXH 7
DB 2 LFFNH 6

RESULT 28
ID 09BYYS PRELIMINARY; PRT; 8 AA.
AC 09BYYS;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618 (2001).
DR EMBL; AY011664; AAG47575.1; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003677; F:DNA binding; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
FT NON TER
SQ SEQUENCE 8 AA; 1006 MW; DF02C331ERAB572A CRC64;

Query Match          40.0%; Score 10; DB 4; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXXVXH 7
DB 1 DLYCH 5

RESULT 29
ID 015893 PRELIMINARY; PRT; 8 AA.
AC 015893;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE (Clone XP587N) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
  arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0 (1995).
DR EMBL; I32073; AAA73883.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;

Query Match          40.0%; Score 10; DB 4; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXH 6
DB 1 SQNPLO 6

RESULT 30
ID 081UB8 PRELIMINARY; PRT; 8 AA.
AC 081UB8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CD95 antigen (Fragment).
GN CD95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22404279; PubMed=12516573;

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RA Kurth J., Pernio A., Schmitz R., Iking-Konert C., Chiorazzi N.,
 RA Thompson K.M., Winkler T., Rajewsky K., Kuipers R.;
 RT "Lack of deleterious somatic mutations in the CD95 gene of
 RT plasmablasts from systemic lupus erythematosus patients and
 RT autotibody-producing cell lines";
 RL Eur. J. Immunol. 32:3785-3792(2002).
 DR EMBL, AJ509178; CAD48928.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 846 MW; 34B724405DC2D1AB CRC64;
 Query Match 40.0%; Score 10; DB 4; Length 8;
 Best Local Similarity 14.3%; Pred. No. 1e+06;
 Matches 1; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QXXVXHL 8
 DB 1 ETVAIHL 7
 RESULT 31
 ID Q8MUN6 PRELIMINARY; PRT; 8 AA.
 AC Q8MUN6;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Mannose phosphate isomerase (Fragment).
 GN MPI.
 OS Heliconius melpomene melpomene.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.
 OC NCBI_TaxID=171917;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=STRI-B-441-Mpi-2;
 RA Bull V., Beltran M., Berningham E., Jiggins C., McMillan O.,
 RA Mallet J.;
 RT "Molecular evidence for gene flow between species of Heliconius";
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF516247; AAM61933.1; -.
 DR GO: GO:0016553; F:isomerase activity; IEA.
 KW isomerase.
 FT NON TER 1 1
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 977 MW; 16E736DB1DD1EAA3 CRC64;
 Query Match 40.0%; Score 10; DB 5; Length 8;
 Best Local Similarity 14.3%; Pred. No. 1e+06;
 Matches 1; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 XQXXVXH 7
 DB 2 DHAEQLH 8
 RESULT 32
 ID 002032 PRELIMINARY; PRT; 8 AA.
 AC 002032;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE Metallothionein (Fragment).
 GN LPM12.
 OS Lytechinus pictus (Painted sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
 OC Echinoidea.
 OC NCBI_TaxID=7653;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=97264487; PubMed=9110313;
 RA Cserjesi P., Fang H., Brandhorst B.P.;
 RT "Metallothionein gene expression in embryos of the sea urchin
 RT Lytechinus pictus";
 RL Mol. Reprod. Dev. 47:39-46(1997).
 DR EMBL, U83400; AAB58320.1; -.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 823 MW; EBD5A2C1F7686766 CRC64;
 Query Match 40.0%; Score 10; DB 5; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 6 XHL 8
 DB 4 PHV 6
 RESULT 33
 ID 086BS9 PRELIMINARY; PRT; 8 AA.
 AC 086BS9;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Cyclin B (Fragment).
 GN Cyclin B.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Strongylocentrotidae;
 OC Strongylocentrotus.
 OC NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96027756; PubMed=7546293;
 RA Thatcher J.D., McBride B., Katula K.S.;
 RT "Promoter binding factors regulating cyclin B transcription in the sea
 RT urchin embryo";
 RL DNA Cell Biol. 14:869-881(1995).
 DR EMBL, S80441; AAP32224.1; -.
 KW Cyclin.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 897 MW; EE645411ADD1EDD6 CRC64;
 Query Match 40.0%; Score 10; DB 5; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 5 VXH 7
 DB 1 MAH 3
 RESULT 34
 ID 09TT78 PRELIMINARY; PRT; 8 AA.
 AC 09TT78;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Thymidylate synthase (Fragment).
 GN TS.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21015404; PubMed=11130975;
 RA Brouillette J.A., Andrew J.R., Venna P.J.;
 RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
 RT method";
 RL Mamm. Genome 11:1079-1086(2000).

DR EMBL; AF202073; AAF20918.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 899 MW; 6731A1E059CA667 CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
:::|
Db 2 GDFIH 6

RESULT 35

ID Q9BF82 PRELIMINARY; PRT; 8 AA.
AC Q9BF82;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Ursus arctos (Brown bear) (Grizzly bear).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=9644;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals."
RL Nature 409:614-618(2001).
DR EMBL; AY011683; AAG47591.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
:::|
Db 1 DLYCH 5

RESULT 36

ID Q9BFC2 PRELIMINARY; PRT; 8 AA.
AC Q9BFC2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Macropus eugenii (Tamar wallaby).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals."
RL Nature 409:614-618(2001).
DR EMBL; AY011621; AAG47536.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;

Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 XXVXH 7
:::|
Db 1 DLYCH 5

RESULT 37

ID Q9BF90 PRELIMINARY; PRT; 8 AA.
AC Q9BF90;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Tragelaphus eurycerus (Bongo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Tragelaphus.
OX NCBI_TaxID=69297;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals."
RL Nature 409:614-618(2001).
DR EMBL; AY011673; AAG47583.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
:::|
Db 1 DLYCH 5

RESULT 38

ID Q9BFB1 PRELIMINARY; PRT; 8 AA.
AC Q9BFB1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Echinos telfairi (lesser hedgehog tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Echinos.
OX NCBI_TaxID=9371;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals."
RL Nature 409:614-618(2001).
DR EMBL; AY011632; AAG47547.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
:::|
Db 1 DLYCH 5

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RESULT 39
Q9BFA1 ID Q9BFA1 PRELIMINARY; PRT; 8 AA.
AC Q9BFA1;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Ateles fusciceps (Brown-headed epider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.
OX NCBI_TaxID=9508;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011660; AAC47571.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 40
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AC Q9BF87;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Tapirus indicus (Asiatic tapir) (Malayan tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perisodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=9802;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011678; AAC47586.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 41
Q9BFB9 ID Q9BFB9 PRELIMINARY; PRT; 8 AA.
AC Q9BFB9;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)

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DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Euphractus sexinctus (Six-banded armadillo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Euphractus.
OX NCBI_TaxID=143300;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011624; AAC47539.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 42
Q9BFB8 ID Q9BFB8 PRELIMINARY; PRT; 8 AA.
AC Q9BFB8;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Chaetophactus villosus (South American armadillo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophactus.
OX NCBI_TaxID=29080;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011625; AAC47540.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 43
Q9BFA0 ID Q9BFA0 PRELIMINARY; PRT; 8 AA.
AC Q9BFA0;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OC Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.

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OX NCBI_TaxID=9544;
RN [1]
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RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011631; AAC47572.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 1006 MW; DF02C311EAB572A CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 XXVXH 7
DB 1 DLYCH 5

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RESULT 44
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AC Q9BFA8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM
OS Loxodonta africana (African elephant).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Loxodonta.
OX NCBI_TaxID=9785;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011635; AAC47550.1; -.
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SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

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Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 XXVXH 7
DB 1 DLYCH 5

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RESULT 45
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AC Q9BFA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM
OS Procaravia capensis (Cape hyrax) (Rock dassie).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Hyracoidea; Procaviidae; Procavia.
OX NCBI_TaxID=9813;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";

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RL Nature 409:614-618(2001).
DR EMBL; AY011634; AAC47549.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 XXVXH 7
DB 1 DLYCH 5

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Search completed: August 19, 2004, 15:50:49
Job time : 32 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 19, 2004, 15:47:57 ; Search time 13.5 Seconds
(Without alignments)
30.593 Million cell updates/sec

Title: VARIANT2
Perfect score: 25
Sequence: 1 XQXXVXHI 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 13858

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	25	100.0	8 4 US-09-248-381-18	Sequence 18, Appl
2	25	100.0	8 4 US-09-248-381-19	Sequence 11, Appl
3	23	92.0	8 1 US-08-168-390-11	Sequence 12, Appl
4	23	92.0	8 1 US-08-168-390-12	Sequence 9, Appl
5	23	92.0	8 2 US-08-337-127-9	Sequence 9, Appl
6	23	92.0	8 4 US-09-260-846-9	Sequence 16, Appl
7	23	92.0	8 4 US-09-248-381-16	Sequence 17, Appl
8	23	92.0	8 4 US-09-248-381-17	Patent No. 5217955
9	23	92.0	8 6 5217955-32	Patent No. 5217955
10	23	92.0	8 6 5217955-34	Patent No. 5217955
11	23	92.0	8 6 5217955-35	Patent No. 5217955
12	23	92.0	8 6 5217955-36	Patent No. 5217955
13	23	92.0	8 1 US-08-031-325A-27	Sequence 27, Appl
14	21	84.0	8 2 US-08-337-127-4	Sequence 4, Appl
15	21	84.0	8 2 US-08-337-127-8	Sequence 8, Appl
16	21	84.0	8 4 US-09-260-846-4	Sequence 4, Appl
17	21	84.0	8 4 US-09-260-846-8	Sequence 6, Appl
18	21	84.0	8 4 US-09-248-381-6	Sequence 6, Appl
19	21	84.0	8 6 5217955-31	Patent No. 5217955
20	21	84.0	8 6 5217955-33	Patent No. 5217955
21	21	84.0	8 6 5217955-38	Patent No. 5217955
22	20	80.0	8 3 US-08-444-818-632	Sequence 632, App
23	20	80.0	8 6 5217955-37	Patent No. 5217955
24	19	76.0	8 3 US-08-444-818-633	Sequence 633, App
25	18	72.0	8 1 US-08-168-390-13	Sequence 13, Appl
26	18	72.0	8 1 US-08-168-390-14	Sequence 14, Appl
27	18	72.0	8 1 US-08-178-268-16	Sequence 16, Appl

28	18	72.0	8 3 US-09-082-279B-1459	Sequence 1459, Ap
29	18	72.0	8 4 US-09-315-304B-1612	Sequence 1612, Ap
30	18	72.0	8 4 US-09-834-784-1459	Sequence 1459, Ap
31	18	72.0	8 4 US-09-350-641C-1613	Sequence 1613, Ap
32	17	68.0	8 1 US-08-387-634-3	Sequence 3, Appl
33	17	68.0	8 3 US-08-816-346-20	Sequence 20, Appl
34	17	68.0	8 4 US-09-335-411-20	Sequence 20, Appl
35	17	68.0	8 3 US-09-515-965A-1846	Sequence 1846, Ap
36	17	68.0	8 6 5217955-25	Patent No. 5217955
37	17	68.0	8 6 5217955-27	Patent No. 5217955
38	17	68.0	8 6 5217955-28	Patent No. 5217955
39	16	64.0	8 1 US-08-457-804-5	Sequence 5, Appl
40	16	64.0	8 1 US-08-843-035-16	Sequence 16, Appl
41	16	64.0	8 1 US-08-178-268-10	Sequence 10, Appl
42	16	64.0	8 2 US-07-885-089B-25	Sequence 25, Appl
43	16	64.0	8 2 US-08-755-496A-16	Sequence 16, Appl
44	16	64.0	8 3 US-08-525-002-37	Sequence 37, Appl
45	16	64.0	8 3 US-08-444-818-432	Sequence 432, App

ALIGNMENTS

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RESULT 1
US-09-248-381-18
; Sequence 18, Application US/09248381
; Patent No. 6492330
; GENERAL INFORMATION:
; APPLICANT: MUKHERJEE, RAMA
; APPLICANT: JAGGI, MANU
; APPLICANT: PRASAD, SUDHANAND
; APPLICANT: BURMAN, ANAND C
; APPLICANT: RAJENDRAN, PRAVEEN
; APPLICANT: MATHER, ARCHANA
; APPLICANT: SINGH, ANU T
; TITLE OF INVENTION: ANTITUMORIC DRUGS
; FILE REFERENCE: U 011695-8
; CURRENT APPLICATION NUMBER: US/09/248,381
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This peptide
; OTHER INFORMATION: was synthetically generated.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb
; US-09-248-381-18

Query Match      100.0%; Score 25; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. NO. 3e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 XQXXVXHI 8
Db      1 XQXXVXHI 8

RESULT 2
US-09-248-381-19
; Sequence 19, Application US/09248381
; Patent No. 6492330
; GENERAL INFORMATION:
; APPLICANT: MUKHERJEE, RAMA

```

```

/ APPLICANT: JAGGI, MANU
/ APPLICANT: PRASAD, SUDHANAND
/ APPLICANT: BURMAN, ANAND C
/ APPLICANT: RAJENDRAN, PRAVEEN
/ APPLICANT: MATHEUR, ARCHANA
/ APPLICANT: SINGH, ANU T
/ TITLE OF INVENTION: ANTIANGIOGENIC DRUGS
/ FILE REFERENCE: U 011695-8
/ CURRENT APPLICATION NUMBER: US/09/248,381
/ CURRENT FILING DATE: 1999-02-11
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: This peptide
/ OTHER INFORMATION: was synthetically generated.
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)-
/ OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
/ NAME/KEY: MOD_RES
/ LOCATION: (6)
/ OTHER INFORMATION: /product=2-amino-4-isobutyric acid/label=Alb
/ US-09-248-381-19

Query Match      100.0%; Score 25; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 XQXXVXHI 8
DB      1 XQWAVVHI 8

RESULT 3
/ US-08-168-390-11
/ Sequence 11, Application US/08168390
/ Patent No. 5620955
/ GENERAL INFORMATION:
/ APPLICANT: Knight, Martha
/ APPLICANT: Takahashi, Kazayuki
/ APPLICANT: Chandrasekhar, Bhaskar
/ TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox
/ STREET: 1100 New York Avenue, Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/168,390
/ FILING DATE: Herewith
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Goldstein, Jorge A.
/ REGISTRATION NUMBER: 29,021
/ REFERENCE/DOCKET NUMBER: 0871.0040001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540
/ TELEX: 248636 SSK
/ OTHER INFORMATION: FOR SEQ ID NO: 11:
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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /note="The amino-terminal residue
/ OTHER INFORMATION: comprises one of several chemical end caps."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 8
/ OTHER INFORMATION: /note="The carboxy-terminal
/ OTHER INFORMATION: residue comprises an ethyl ester."
/ US-08-168-390-11

Query Match      92.0%; Score 23; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 XQXXVXHI 8
DB      1 XQWAVVHI 8

RESULT 4
/ US-08-168-390-12
/ Sequence 12, Application US/08168390
/ Patent No. 5620955
/ GENERAL INFORMATION:
/ APPLICANT: Knight, Martha
/ APPLICANT: Takahashi, Kazayuki
/ APPLICANT: Chandrasekhar, Bhaskar
/ TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox
/ STREET: 1100 New York Avenue, Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/168,390
/ FILING DATE: Herewith
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Goldstein, Jorge A.
/ REGISTRATION NUMBER: 29,021
/ REFERENCE/DOCKET NUMBER: 0871.0040001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540
/ TELEX: 248636 SSK
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /note="The amino-terminal residue
/ OTHER INFORMATION: comprises one of several chemical end caps."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 6
/ OTHER INFORMATION: /note="The alanine at position 6
```

OTHER INFORMATION: is dextrorotatory alanine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /note="The carboxy-terminal
OTHER INFORMATION: residue comprises an ethyl ester."
US-08-168-390-12

Query Match 92.0%; Score 23; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 3; Conservative 5; Mismatches 0;

QY 1 XQXXVXH 8
:|::|:|:
Db 1 NQWAVVHL 8

RESULT 5
US-08-337-127-9
Sequence 9, Application US/08337127
Patent No. 5877277
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Moreau, Jacques-Pierre
APPLICANT: Kim, Sun H.
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
TITLE OF INVENTION: ANALOGS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,127
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/779,039
FILING DATE: 10/18/91
APPLICATION NUMBER: 07/502,438
FILING DATE: 03/30/90
APPLICATION NUMBER: 07/397,169
FILING DATE: 08/21/89
APPLICATION NUMBER: 07/376,555
FILING DATE: 07/07/89
APPLICATION NUMBER: 07/317,941
FILING DATE: 03/02/89
APPLICATION NUMBER: 07/282,328
FILING DATE: 12/09/88
APPLICATION NUMBER: 07/257,998
FILING DATE: 10/14/88
APPLICATION NUMBER: 07/248,771
FILING DATE: 09/23/88
APPLICATION NUMBER: 07/207,759
FILING DATE: 06/16/88
APPLICATION NUMBER: 07/204,171
FILING DATE: 06/08/88
APPLICATION NUMBER: 07/173,311
FILING DATE: 03/25/88
APPLICATION NUMBER: 07/100,571
FILING DATE: 09/24/87
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00537/009000

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The sequence contains at
OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,
OTHER INFORMATION: and has an methyl ester C-terminus (i.e., COYCH3),
OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COYOH).
US-08-337-127-9

Query Match 92.0%; Score 23; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 3; Conservative 5; Mismatches 0;

QY 1 XQXXVXH 8
:|::|:|:
Db 1 EQWAVGHL 8

RESULT 6
US-09-260-846-9
Sequence 9, Application US/09260846
Patent No. 6307017
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Moreau, Jacques-Pierre
APPLICANT: Kim, Sun Hyuk
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
FILE REFERENCE: 00537/009000
CURRENT APPLICATION NUMBER: US/09/260,846
CURRENT FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
US-09-260-846-9

Query Match 92.0%; Score 23; DB 4; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 3; Conservative 5; Mismatches 0;

QY 1 XQXXVXH 8
:|::|:|:
Db 1 EQWAVGHL 8

RESULT 7
US-09-248-381-16
Sequence 16, Application US/09248381
Patent No. 6492330
GENERAL INFORMATION:
APPLICANT: MUKHERJEE, RAMA
APPLICANT: JAGGI, MANU
APPLICANT: PRASAD, SUDHANAND
APPLICANT: BURMAN, ANAND C
APPLICANT: RAJENDRAN, PRAVEEN

```
APPLICANT: MATUR, ARCHANA
APPLICANT: SINGH, ANU T
TITLE OF INVENTION: ANTICANGIOGENIC DRUGS
FILE REFERENCE: U 011695-8
CURRENT APPLICATION NUMBER: US/09/248,381
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: This peptide
OTHER INFORMATION: was synthetically generated.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)_RES
OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe;
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)_
OTHER INFORMATION: /product=2-amino-isobutyric acid/label=aiB
US-09-248-381-16
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Query Match 92.0%; Score 23; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8
DB 1 XQXVGH 8

```
RESULT 8
US-09-248-381-17
Sequence 17, Application US/09248381
Patent No. 6492330
GENERAL INFORMATION:
APPLICANT: MUGHERJEE, RAMA
APPLICANT: JAGGI, MANU
APPLICANT: PRASAD, SUDHANAND
APPLICANT: BURMAN, ANAND C
APPLICANT: RAJENDRAN, PRAVEEN
APPLICANT: MATUR, ARCHANA
APPLICANT: SINGH, ANU T
TITLE OF INVENTION: ANTICANGIOGENIC DRUGS
FILE REFERENCE: U 011695-8
CURRENT APPLICATION NUMBER: US/09/248,381
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: This peptide
OTHER INFORMATION: was synthetically generated.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)_
OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
NAME/KEY: MOD_RES
LOCATION: (6)_RES
OTHER INFORMATION: /product=2-amino-isobutyric acid/label=aiB
US-09-248-381-17
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Query Match 92.0%; Score 23; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8
DB 1 XQXVGH 8

```
RESULT 9
5217955-32
Patent No. 5217955
APPLICANT: ABOGDE, ARTHUR E.;MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO:32
LENGTH: 8
5217955-32
```

Query Match 92.0%; Score 23; DB 6; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8
DB 1 FQWAVGH 8

```
RESULT 10
5217955-34
Patent No. 5217955
APPLICANT: ABOGDE, ARTHUR E.;MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO:34
LENGTH: 8
5217955-34
```

Query Match 92.0%; Score 23; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8
DB 1 XQXVGH 8

```
RESULT 11
5217955-35
Patent No. 5217955
APPLICANT: ABOGDE, ARTHUR E.;MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 440,039
```

FILING DATE: 21-NOV-1989
 APPLICATION NUMBER: 408,125
 FILING DATE: 15-SEP-1989
 SEQ ID NO:35:
 LENGTH: 8
 5217955-35

Query Match 92.0%; Score 23; DB 6; Length 8;
 Best Local Similarity 50.0%; Pred. No. 3e+05;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 XQXXVXHI 8
 Db 1 XQWAVAHL 8

RESULT 12
 5217955-36
 Patent No. 5217955
 APPLICANT: ABOGDE, ARTHUR E.; MOREAU, JACQUES-PIERRE
 TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
 OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
 NUMBER OF SEQUENCES: 42
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/520,225
 FILING DATE: 09-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 440,039
 FILING DATE: 21-NOV-1989
 APPLICATION NUMBER: 408,125
 FILING DATE: 15-SEP-1989
 SEQ ID NO:36:
 LENGTH: 8
 5217955-36

Query Match 92.0%; Score 23; DB 6; Length 8;
 Best Local Similarity 37.5%; Pred. No. 3e+05;
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 XQXXVXHI 8
 Db 1 FQWAVAHL 8

RESULT 13
 US-08-325A-27
 Sequence 27, Application US/08031325A
 Patent No. 5369094
 GENERAL INFORMATION:
 APPLICANT: Schall, Andrew V.
 APPLICANT: Cal, Renzh
 TITLE OF INVENTION: POLYPEPTIDE BOMBESIN ANTAGONISTS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OMRI M. BEHR, ESQ
 STREET: 325 PIERSON AVENUE
 CITY: EDISON
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 08837
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/031,325A
 FILING DATE: 15-MAR-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/619,747
 FILING DATE: 29-NOV-1990
 ATTORNEY/AGENT INFORMATION:

NAME: BEHR, OMRI M.
 REGISTRATION NUMBER: 22,940
 REFERENCE/DOCKET NUMBER: SHAL3-0-014
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 494-5240
 TELEFAX: (908) 494-0428
 TELEX: 511642 BEPATEDIN

INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:

NAME/KEY: misc_feature

LOCATION: 1
 OTHER INFORMATION: /note= "Res 1 = (R1) (R2)-A0-A1, where A0

OTHER INFORMATION: = deleted; A1 = D-Phe, D-Tip or D-Nal; R1 and R2 = H"

NAME/KEY: misc_feature

LOCATION: 8
 OTHER INFORMATION: /note= "Res 8 = A8-N, where N = -N(R8)-

OTHER INFORMATION: CH(Z1)-R4-CH(Z2)-CO-V, where R4 = CH2NH; Z1 = -CH2CH(CH3)2; Z2

OTHER INFORMATION: H or
 OTHER INFORMATION: COEL, where B1 = C1-20 alkyl"

US-08-031-325A-27

Query Match 84.0%; Score 21; DB 1; Length 8;
 Best Local Similarity 57.1%; Pred. No. 3e+05;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 XQXXVXHI 7
 Db 1 XQWAVGH 7

RESULT 14
 US-08-337-127-4
 Sequence 4, Application US/08337127
 Patent No. 5877277
 GENERAL INFORMATION:
 APPLICANT: Coy, David H.
 APPLICANT: Moreau, Jacques-Pierre
 APPLICANT: Kim, Sun H.
 TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 COMPUTER: IBM PS/2 Model 502 or 55SX
 OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 SOFTWARE: NordPerfect (Version 5.0)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/337,127
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/779,039
 FILING DATE: 10/18/91
 APPLICATION NUMBER: 07/502,438
 FILING DATE: 03/30/90
 APPLICATION NUMBER: 07/397,169
 FILING DATE: 08/21/89
 APPLICATION NUMBER: 07/376,555

```

1      FILING DATE: 07/07/89
2      APPLICATION NUMBER: 07/317,941
3      FILING DATE: 03/02/89
4      APPLICATION NUMBER: 07/282,328
5      FILING DATE: 12/09/88
6      APPLICATION NUMBER: 07/257,998
7      FILING DATE: 10/14/88
8      APPLICATION NUMBER: 07/248,771
9      FILING DATE: 09/23/88
10     APPLICATION NUMBER: 07/207,759
11     FILING DATE: 06/16/88
12     APPLICATION NUMBER: 07/204,171
13     FILING DATE: 06/08/88
14     APPLICATION NUMBER: 07/173,311
15     FILING DATE: 03/25/88
16     APPLICATION NUMBER: 07/100,571
17     FILING DATE: 09/24/87
18     ATTORNEY/AGENT INFORMATION:
19     NAME: Clark, Paul T.
20     REGISTRATION NUMBER: 30,162
21     REFERENCE/DOCKET NUMBER: 00537/00900D
22     TELECOMMUNICATION INFORMATION:
23     TELEPHONE: (617) 542-5070
24     TELEFAX: (617) 542-8906
25     TELEX: 200154
26     INFORMATION FOR SEQ ID NO: 4:
27     SEQUENCE CHARACTERISTICS:
28     LENGTH: 8
29     TYPE: amino acid
30     STRANDEDNESS:
31     TOPOLOGY: linear
32     FEATURE:
33     OTHER INFORMATION: The sequence contains at
34     OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,
35     OTHER INFORMATION: and has an amide C-terminus (i.e., COYNH2), rather
36     OTHER INFORMATION: than
37     OTHER INFORMATION: a carboxyl C-terminus (i.e., COYOH). Xaa strands for
38     OTHER INFORMATION: staline.
39     GS-08-337-127-4

```

```

QY      1 XQXVXH 7
       :|::|:|
Db      1 EQWAVGH 7

RESULT 15
; Sequence 8, Application US/0837127
; Patent No. 5877277
; GENERAL INFORMATION:
; APPLICANT: COY, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun H.
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 555X
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/337,127
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/779,039
FILING DATE: 10/18/91
APPLICATION NUMBER: 07/502,438
FILING DATE: 03/30/90
APPLICATION NUMBER: 07/397,169
FILING DATE: 08/21/89
APPLICATION NUMBER: 07/376,555
FILING DATE: 07/07/89
APPLICATION NUMBER: 07/317,941
FILING DATE: 03/02/89
APPLICATION NUMBER: 07/282,328
FILING DATE: 12/09/88
APPLICATION NUMBER: 07/257,998
FILING DATE: 10/14/88
APPLICATION NUMBER: 07/248,771
FILING DATE: 09/23/88
APPLICATION NUMBER: 07/207,759
FILING DATE: 06/16/88
APPLICATION NUMBER: 07/204,171
FILING DATE: 06/08/88
APPLICATION NUMBER: 07/173,311
FILING DATE: 03/25/88
APPLICATION NUMBER: 07/100,571
FILING DATE: 09/24/87
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00537/00900D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The sequence contains at
OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,
OTHER INFORMATION: and has an methyl-ester C-terminus (i.e., COOCH3),
OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COOH).
IS-08-337-127-8

```

QY      1  XXXXXXX 7
      : ::|:|
Db      1  EQMAVGH 7

      84.0%; Score 21; DB 2; Length 8;
Query Match Similarity 42.9%; Pred. No. 3e+05;
Best Local Similarity 42.9%; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 4;

RESULT 16
US-09-260-846-4
; Sequence 4, Application US/09260846
; Patent No. 6307017
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun Hyuk
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
; FILE REFERENCE: 00537/00900J
; CURRENT APPLICATION NUMBER: US/09/260,846
; CURRENT FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4

```

```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: pyroglutamate
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: statine
; FEATURE:
; OTHER INFORMATION: this peptide has an amidated c-terminus
US-09-260-846-4

Query Match
Best Local Similarity 84.0%; Score 21; DB 4; Length 8;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXH 7
   ||::||
Db 1 EQWAVGH 7

RESULT 17
US-09-260-846-8
; Sequence 8, Application US/09260846
; Patent No. 6307017
; GENERAL INFORMATION:
; APPLICANT: COV, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun Hyuk
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
; FILE REFERENCE: 00537/00900J
; CURRENT APPLICATION NUMBER: US/09/260,846
; CURRENT FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: pyroglutamate
; FEATURE:
; OTHER INFORMATION: this peptide has a methyl ester c-terminus
US-09-260-846-8

Query Match
Best Local Similarity 84.0%; Score 21; DB 4; Length 8;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXH 7
   ||::||
Db 1 EQWAVGH 7

RESULT 18
US-09-248-381-6
; Sequence 6, Application US/09248381
; Patent No. 6492310
; GENERAL INFORMATION:
; APPLICANT: MURKROE, RAMA
; APPLICANT: JAGGI, MANU
; APPLICANT: PRASAD, SUDHANAND
; APPLICANT: BURMAN, ANAND C
; APPLICANT: RAJENDRAN, PRAVEEN
```

```
; APPLICANT: MATHUR, ARCHANA
; APPLICANT: SINGH, ANU T
; TITLE OF INVENTION: ANTITUMORIGENIC DRUGS
; FILE REFERENCE: U:011695-8
; CURRENT APPLICATION NUMBER: US/09/248,381
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This peptide
; OTHER INFORMATION: was synthetically generated.
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION:
US-09-248-381-6

Query Match
Best Local Similarity 84.0%; Score 21; DB 4; Length 8;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXH 7
   ||::||
Db 1 XQWAVGH 7

RESULT 19
5217955-31
; Patent No. 5217955
; APPLICANT: ABOGDE, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:31;
; LENGTH: 8
5217955-31

Query Match
Best Local Similarity 84.0%; Score 21; DB 6; Length 8;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXH 7
   ||::||
Db 1 XQWAVGH 7

RESULT 20
5217955-33
; Patent No. 5217955
; APPLICANT: ABOGDE, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO:33
LENGTH: 8
5217955-33

Query Match 84.0%; Score 21; DB 6; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXH 7
Db 1 EQWAVGH 7

RESULT 21
5217955-38
Patent No. 5217955
APPLICANT: ABOGDE, ARTHUR E.; MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO:38;
LENGTH: 8
5217955-38

Query Match 84.0%; Score 21; DB 6; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXH 7
Db 1 EQWAVGH 7

RESULT 22
US-08-444-818-632
Sequence 632, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 632:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-632

Query Match 80.0%; Score 20; DB 3; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHI 8
Db 1 RKAIVTHI 7

RESULT 23
5217955-37
Patent No. 5217955
APPLICANT: ABOGDE, ARTHUR E.; MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO:37;
LENGTH: 8
5217955-37

Query Match 80.0%; Score 20; DB 6; Length 8;
Best Local Similarity 25.0%; Pred. No. 3e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXHI 8
Db 1 FEWAVVHL 8

RESULT 24
US-08-444-818-633
Sequence 633, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hardin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 633:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-633

Query Match 76.0%; Score 19; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHI 8
Db 1 KAVTHI 6

RESULT 25
US-08-168-390-13
Sequence 13, Application US/08168390
Patent No. 5620955
GENERAL INFORMATION:
APPLICANT: Knight, Martha
APPLICANT: Takahashi, Kazayuki
APPLICANT: Chandrasekhar, Bhaskar
TITLE OF INVENTION: Bombesin/Gastatin Releasing Peptide Antagonists
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,390
FILING DATE: Herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0871.0040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:

NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "The amino-terminal residue
OTHER INFORMATION: comprises one of several chemical end caps."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /note= "The carboxy-terminal
OTHER INFORMATION: residue comprises an ethyl ester."
US-08-168-390-13

Query Match 72.0%; Score 18; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 3e+05;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8
Db 1 NHWVGH 8

RESULT 26
US-08-168-390-14
Sequence 14, Application US/08168390
Patent No. 5620955
GENERAL INFORMATION:
APPLICANT: Knight, Martha
APPLICANT: Takahashi, Kazayuki
APPLICANT: Chandrasekhar, Bhaskar
TITLE OF INVENTION: Bombesin/Gastatin Releasing Peptide Antagonists
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,390
FILING DATE: Herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0871.0040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "The amino-terminal residue
OTHER INFORMATION: comprises one of several chemical end caps."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note= "The alanine at position 6
OTHER INFORMATION: is dextrorotatory alanine."
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /note= "The carboxy-terminal

OTHER INFORMATION: residue comprises an ethyl ester."

US-08-168-390-14

Query Match

72.0%; Score 18; DB 1; Length 8;

Best Local Similarity 25.0%; Pred. No. 3e+05;

Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8
: : : : :
Db 1 NHWVAHL 8

RESULT 27

US-08-178-268-16

Sequence 16, Application US/08178268

Patent No. 5795859

GENERAL INFORMATION:

APPLICANT: RATHGEN, Deborah A

APPLICANT: WIDMER, Fred

APPLICANT: GRIGG, Geoffrey W

APPLICANT: MACK, Philip O

TITLE OF INVENTION: Peptide which Abrogates TNF and/or LPS Toxicity

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSER: Nixon & Vanderhye P.C.

STREET: 1100 No. 5795859th Glebe Road, 8th Floor

CITY: Arlington

STATE: Virginia

COUNTRY: USA

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/178,268

FILING DATE: 05-JAN-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: MITCHARD, Leonard C

REGISTRATION NUMBER: 29,009

REFERENCE/DOCKET NUMBER: 47-45

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: both

MOLECULE TYPE: peptide

US-08-178-268-16

Query Match

72.0%; Score 18; DB 1; Length 8;

Best Local Similarity 33.3%; Pred. No. 3e+05;

Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHI 8
: : : : :
Db 1 KPVAHV 6

RESULT 28

US-09-082-279B-1459

Sequence 1459, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1459

LENGTH: 8

TYPE: PRT

ORGANISM: HIV-1

US-09-082-279B-1459

Query Match

72.0%; Score 18; DB 3; Length 8;

Best Local Similarity 37.5%; Pred. No. 3e+05;

Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8
: : : : :
Db 1 WOQWDQHI 8

RESULT 29

US-09-315-304B-1612

Sequence 1612, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1612

LENGTH: 8

TYPE: PRT

ORGANISM: HIV-1

US-09-315-304B-1612

Query Match

72.0%; Score 18; DB 4; Length 8;

Best Local Similarity 37.5%; Pred. No. 3e+05;

Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8
: : : : :
Db 1 WOQWDQHI 8

RESULT 30

US-09-834-784-1459

Sequence 1459, Application US/09834784

Patent No. 6362787

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/834,784

CURRENT FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1459
LENGTH: 8
TYPE: PRT
ORGANISM: HIV-1
US-09-834-784-1459

Query Match 72.0%; Score 18; DB 4; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8
:|:|:|
DB 1 WQWMDQHI 8

RESULT 31
US-09-350-641C-1613
Sequence 1613 Application US/09350641C
Patent No. 6656906
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-067
CURRENT APPLICATION NUMBER: US/09/350,641C
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1613
LENGTH: 8
TYPE: PRT
ORGANISM: HIV-1
US-09-350-641C-1613

Query Match 72.0%; Score 18; DB 4; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8
:|:|:|
DB 1 WQWMDQHI 8

RESULT 32
US-08-387-634-3
Sequence 3 Application US/08387634
Patent No. 5767236
GENERAL INFORMATION:
APPLICANT: Kim, Sun Hyuk
APPLICANT: Moreau, Jacques-Pierre
TITLE OF INVENTION: LINEAR THERAPEUTIC PEPTIDES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,634
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/929,306A
FILING DATE: 08/13/92
APPLICATION NUMBER: US/07/520,226
FILING DATE: 05/09/90
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T. and Tsao, Y. Rocky
REGISTRATION NUMBER: 30,162 and 34,053
REFERENCE/DOCKET NUMBER: 00537/040002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
FEATURE:
OTHER INFORMATION:
OTHER INFORMATION: The sequence contains at position 1 an acetylated His, rather
than a His, and has an amide C-terminus (i.e., COOH).
US-08-387-634-3

Query Match 68.0%; Score 17; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHI 8
:|:|:|
DB 2 WAVGHL 7

RESULT 33
US-08-816-346-20
Sequence 20 Application US/08816346
Patent No. 6127525
GENERAL INFORMATION:
APPLICANT: Crystal, Ronald G.
APPLICANT: Falck-Pedersen, Erik
APPLICANT: Gall, Jason
APPLICANT: Kovsedl, Imre
APPLICANT: Wickham, Thomas J.
TITLE OF INVENTION: CHIMERIC ADENO VIRAL COAT PROTEIN AND
METHODS OF USING SAME
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #110, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,346
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 67167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/616-5600

TELEFAX: 312/616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-816-346-20

Query Match
Best Local Similarity 68.0%; Score 17; DB 3; Length 8;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXH 7
Db 1 YETEHNH 7

RESULT 34
US-09-335-411-20

Sequence 20, Application US/09335411
Patent No. 6153435

GENERAL INFORMATION:

APPLICANT: Crystal, Ronald G.
APPLICANT: Falck-Pedersen, Erik

APPLICANT: Gall, Jason

APPLICANT: Kovesam, Imre

APPLICANT: Wickham, Thomas J.

TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND
METHODS OF USING SAME

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA - 4900
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60601-6780

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/335,411

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/816,346

FILING DATE:

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 67167

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/616-5600

TELEFAX: 312/616-5700

TELEX: 25-3533

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-335-411-20

Query Match
Best Local Similarity 68.0%; Score 17; DB 3; Length 8;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXH 7
Db 1 YETEHNH 7

RESULT 35
US-09-515-965A-1846
Sequence 1846, Application US/09515965A
Patent No. 6623741

GENERAL INFORMATION:

APPLICANT: Antczak, J.

APPLICANT: Delmedico, M.

APPLICANT: Erickson, J.

APPLICANT: Lambert, D.

APPLICANT: Sista, P.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION

FILE REFERENCE: 7872-073

CURRENT FILING DATE: 2000-02-29

PRIOR APPLICATION NUMBER: 09/315,304

PRIOR FILING DATE: 1998-05-20

PRIOR APPLICATION NUMBER: 09/082,279

NUMBER OF SEQ ID NOS: 1994

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1846

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide
US-09-515-965A-1846

Query Match
Best Local Similarity 68.0%; Score 17; DB 4; Length 8;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 8
Db 3 SKVLHL 8

RESULT 36
5217955-25

Patent No. 5217955

APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE

TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN

NUMBER OF SEQUENCES: 42

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/520,225

FILING DATE: 09-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 440,039

FILING DATE: 21-NOV-1989

APPLICATION NUMBER: 408,125

FILING DATE: 15-SEP-1989

SEQ ID NO: 25

LENGTH: 8

5217955-25

Query Match
Best Local Similarity 68.0%; Score 17; DB 6; Length 8;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 8
Db 2 WAAVHL 7

RESULT 37
5217955-27

Patent No. 5217955

APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN

NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO: 27
LENGTH: 8
5217955-27

Query Match 68.0%; Score 17; DB 6; Length 8;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH1 8
: : : :
Db 2 WVGHL 7

RESULT 38
5217955-28
Patent No. 5217955
APPLICANT: ABOGDEH, ARTHUR E.; MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEURMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO: 28
LENGTH: 8
5217955-28

Query Match 68.0%; Score 17; DB 6; Length 8;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH1 8
: : : :
Db 2 WVGHL 7

RESULT 39
US-08-457-804-5
Sequence 5, Application US/08457804
Patent No. 5618785
GENERAL INFORMATION:
APPLICANT: Heaver, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
TITLE OF INVENTION: Peptide Inhibitors of Selectin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5618785tlb
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,804
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/156,415
FILING DATE: No. 5618785ember 22, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Diane B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/DOCKET NUMBER: CCOR-0136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-457-804-5

Query Match 64.0%; Score 16; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH1 8
: : : :
Db 2 TKLVH1 7

RESULT 40
US-08-843-035-16
Sequence 16, Application US/0843035
Patent No. 5783662
GENERAL INFORMATION:
APPLICANT: Janney, Paul A.
APPLICANT: Cunningham, C. Casey
APPLICANT: Hartwig, John H.
APPLICANT: Stossel, Thomas P.
APPLICANT: Vegner, Roland
TITLE OF INVENTION: POLYPHOSPHONOSITIDE BINDING
TITLE OF INVENTION: PEPTIDES FOR INTRACELLULAR DRUG DELIVERY
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: Federal Reserve Plaza, 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,035
FILING DATE: 11-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/394,027
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-843-035-16

Query Match 64.0%; Score 16; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
:::|:|
DB 1 KILVXH 6

RESULT 41
US-08-178-268-10
Sequence 10, Application US/08178268
Patent No. 5795859
GENERAL INFORMATION:
APPLICANT: RATHGEN, Deborah A
APPLICANT: WIDMER, Fred
APPLICANT: GRIGG, Geoffrey W
APPLICANT: MACK, Philip O
TITLE OF INVENTION: Peptide which Abrogates TNF and/or LPS Toxicity
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSER: Nixon & Vanderhye P.C.
STREET: 1100 No. 5795859th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178,268
FILING DATE: 05-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, Leonard C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-178-268-10

Query Match 64.0%; Score 16; DB 1; Length 8;
Best Local Similarity 28.6%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXH 7
:::|:|
DB 2 SDXPVXH 8

RESULT 42
US-07-885-089B-25
Sequence 25, Application US/07885089B
Patent No. 5830995

GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: McDonald, Vicki L.
APPLICANT: Bradley, James G.
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: AMPHIREGLINS. A FAMILY OF
TITLE OF INVENTION: HEPARIN-BINDING EPITHELIAL CELL GROWTH FACTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: Penile & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,089B
FILING DATE: 18-MAY-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5624-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-885-089B-25

Query Match 64.0%; Score 16; DB 2; Length 8;
Best Local Similarity 28.6%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXH 7
:::|:|
DB 1 FQNFCH 7

RESULT 43
US-08-755-496A-16
Sequence 16, Application US/08755496A
Patent No. 5846743

GENERAL INFORMATION:
APPLICANT: Cunningham, Casey
APPLICANT: Hartwig, John H.
APPLICANT: Janney, Paul A.
APPLICANT: Stossel, Thomas P.
APPLICANT: Vegners, Roland
TITLE OF INVENTION: POLYPHOSPHOINOSTITIDE-(PI-) BINDING
TITLE OF INVENTION: PEPTIDE(S) FOR INTRACELLULAR DRUG DELIVERY
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSER: Wolf, Greenfield & Sacke, P.C.
STREET: Federal Reserve Plaza, 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,496A
; FILING DATE: 22-NOV-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/394,027
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-755-496A-16

Query Match          64.0%; Score 16; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      2 QXXVXH 7
       ::::|
Db      1 KILVKH 6

RESULT 44
US-08-925-002-37
; Sequence 37, Application US/08925002
; Patent No. 6048527
; GENERAL INFORMATION:
; APPLICANT: Granoff, Dan M.
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
; FILE REFERENCE: 1238, 002
; CURRENT APPLICATION NUMBER: US/08/925,002
; CURRENT FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence from
; OTHER INFORMATION: a phage display peptide library
US-08-925-002-37

Query Match          64.0%; Score 16; DB 3; Length 8;
Best Local Similarity 28.6%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 XQXXVXH 7
       ::::|
Db      1 LNFKVRH 7

RESULT 45
US-08-444-818-432
; Sequence 432, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
```

```

; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hardin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110,002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 432:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-444-818-432

Query Match          64.0%; Score 16; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 XXVXHI 8
       ::::|
Db      3 IGLIHI 8

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Job time : 13.5 secs
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OM protein - protein search, using SW model

Run on: August 19, 2004, 15:51:28 ; Search time 38 Seconds
(without alignments)
66.159 Million cell updates/sec

Title: VARIANT2
Perfect score: 25
Sequence: 1 XQXXVXHI 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 16665

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	92.0	8	10	US-09-896-903C-2
2	23	92.0	8	14	US-10-182-252A-2
3	23	92.0	8	16	US-10-182-252A-2
4	22	88.0	8	9	US-09-766-347-1
5	22	88.0	8	10	US-09-898-887B-1
6	22	88.0	8	14	US-10-281-840-2
7	22	88.0	8	16	US-10-341-577-1
8	21	84.0	8	14	US-10-004-530A-4
9	19	76.0	8	12	US-10-182-252A-332
10	19	76.0	8	12	US-10-182-252A-940
11	19	76.0	8	12	US-10-182-252A-941
12	19	76.0	8	12	US-10-182-252A-942
13	19	76.0	8	12	US-10-182-252A-943
14	19	76.0	8	12	US-10-182-252A-944
15	19	76.0	8	12	US-10-182-252A-946

16	19	76.0	8	12	US-10-182-252A-947	Sequence 947, App
17	19	76.0	8	12	US-10-182-252A-948	Sequence 948, App
18	19	76.0	8	12	US-10-182-252A-950	Sequence 950, App
19	19	76.0	8	12	US-10-182-252A-951	Sequence 951, App
20	19	76.0	8	12	US-10-182-252A-1285	Sequence 1285, App
21	18	72.0	8	12	US-10-387-957-6	Sequence 6, App11
22	18	72.0	8	14	US-10-351-641-1613	Sequence 1613, App
23	18	72.0	8	16	US-10-387-934-6	Sequence 6, App11
24	17	68.0	8	10	US-09-876-904A-181	Sequence 181, App
25	17	68.0	8	12	US-10-387-957-7	Sequence 7, App11
26	17	68.0	8	12	US-10-014-340-64	Sequence 64, App1
27	17	68.0	8	12	US-10-182-252A-624	Sequence 624, App
28	17	68.0	8	12	US-10-182-252A-625	Sequence 625, App
29	17	68.0	8	12	US-10-328-953-94	Sequence 94, App1
30	17	68.0	8	12	US-10-367-580-186	Sequence 186, App
31	17	68.0	8	12	US-10-367-593-234	Sequence 234, App
32	17	68.0	8	12	US-10-367-593-186	Sequence 186, App
33	17	68.0	8	12	US-10-367-593-234	Sequence 234, App
34	17	68.0	8	12	US-10-367-594-186	Sequence 186, App
35	17	68.0	8	12	US-10-367-594-234	Sequence 234, App
36	17	68.0	8	12	US-10-367-654-186	Sequence 186, App
37	17	68.0	8	12	US-10-367-654-234	Sequence 234, App
38	17	68.0	8	12	US-10-367-658-186	Sequence 186, App
39	17	68.0	8	12	US-10-367-658-234	Sequence 234, App
40	17	68.0	8	12	US-10-367-668-186	Sequence 186, App
41	17	68.0	8	12	US-10-367-668-234	Sequence 234, App
42	17	68.0	8	14	US-10-139-146-66	Sequence 66, App1
43	17	68.0	8	14	US-10-052-578-13	Sequence 13, App1
44	17	68.0	8	14	US-10-053-520-13	Sequence 13, App1
45	17	68.0	8	14	US-10-053-498B-13	Sequence 13, App1

ALIGNMENTS

RESULT 1
US-09-896-903C-2
Sequence 2, Appl1
Publication No. US20030050233A1
GENERAL INFORMATION:
APPLICANT: Butman, Anand C.
APPLICANT: Mukherjee, Rama
APPLICANT: Prasad, Suchanand
APPLICANT: Jaggi, Manu
TITLE OF INVENTION: PEPTIDE COMBINATION FOR TREATMENT OF CANCER
FILE REFERENCE: 0132970
CURRENT APPLICATION NUMBER: US/09/896,903C
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: This peptide
OTHER INFORMATION: was synthetically generated.
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)
OTHER INFORMATION: /product = Butanoyl D-phenylalanine/label =
OTHER INFORMATION: Butanoyl-D-Phe
FEATURE:
NAME/KEY: MOD RES
LOCATION: (6)
OTHER INFORMATION: / product = alpha-Aminoisobutyric acid/label = Alb
US-09-896-903C-2
Query Match 92.0%; Score 23; DB 10; Length 8;
Best Local Similarity 62.5%; Pred: No. 1.2e+06;
Matches 5; Conservative 3; Mismatches 0; Gaps 0;

Qy 1 XQXXVXHI 8
Db 1 XQWAVXHL 8

RESULT 2

US-10-186-226A-2
Sequence 2, Application US/10186226A
Publication No. US20030105009A1
GENERAL INFORMATION:
APPLICANT: Prasad, Sudhanand
APPLICANT: Mukherjee, Rama
APPLICANT: Burman, Anand C.
APPLICANT: Mathur, Archana
APPLICANT: Sharma, Rajan
APPLICANT: Jaggi, Manu
TITLE OF INVENTION: POLYPEPTIDES OF COVALENTLY LINKED SYNTHETIC BIOACTIVE PEPTIDE ANA
TITLE OF INVENTION: FOR TREATMENT OF CANCER
FILE REFERENCE: U 014073-7
CURRENT APPLICATION NUMBER: US/10/186,226A
CURRENT FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: This peptide was synthetically generated
NAME/KEY: MISC FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: /product = D-Phenylalanine/label = D-Phe
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: /product = Alpha-amino-isobutyric acid/label = Alb
US-10-186-226A-2

Query Match
Best Local Similarity 92.0%; Score 23; DB 14; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXXVXHI 8
Db 1 XQWAVXHL 8

RESULT 3

US-10-329-321A-2
Sequence 2, Application US/10329321A
Publication No. US20040121950A1
GENERAL INFORMATION:
APPLICANT: Mukherjee, Rama
APPLICANT: Burman, Anand
APPLICANT: Singh, Anu
APPLICANT: Jaggi, Manu
APPLICANT: Prasad, Sudhanand
APPLICANT: Dutt, Sarjana
TITLE OF INVENTION: A DRUG COMPRISING SYNTHETIC PEPTIDE ANALOGS FOR THE TREATMENT OF
TITLE OF INVENTION: CANCER
FILE REFERENCE: U 014319-1
CURRENT APPLICATION NUMBER: US/10/329,321A
CURRENT FILING DATE: 2002-12-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: This peptide was synthetically generated
FEATURE:

NAME/KEY: MISC FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: /product = D-phenylalanine/label = D-Phe
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: /product = 2-amino-isobutyric acid/label = Alb
US-10-329-321A-2

Query Match
Best Local Similarity 92.0%; Score 23; DB 16; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXXVXHI 8
Db 1 XQWAVXHL 8

RESULT 4

US-09-766-347-1
Sequence 1, Application US/09766347
Patent No. US20020169107A1
GENERAL INFORMATION:
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Cantrell, Gary
APPLICANT: Achilefu, Samuel
APPLICANT: Bugaj, Joseph
APPLICANT: Dorschow, Richard
APPLICANT: Mallinckrodt Inc.
TITLE OF INVENTION: NOVEL AROMATIC AZIDES FOR TYPE I PHOTOTHERAPY
FILE REFERENCE: MRD-60
CURRENT APPLICATION NUMBER: US/09/766,347
CURRENT FILING DATE: 2001-01-19
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patent In Version 3.1
SEQ ID NO 1
LENGTH: 8
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(8)
OTHER INFORMATION: Bombesin analog
US-09-766-347-1

Query Match
Best Local Similarity 88.0%; Score 22; DB 9; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.2e+06;

Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXXVXHI 8
Db 1 QWAVGHL 7

RESULT 5

US-09-898-887B-1
Sequence 1, Application US/09898887B
Publication No. US20030158127A1
GENERAL INFORMATION:
APPLICANT: Mallinckrodt Inc.
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Cantrell, Gary
APPLICANT: Achilefu, Samuel I.
APPLICANT: Bugaj, Joseph
APPLICANT: Dorschow, Richard
TITLE OF INVENTION: AROMATIC SULFONATES FOR TYPE I PHOTOTHERAPY
FILE REFERENCE: MRD-61
CURRENT APPLICATION NUMBER: US/09/898,887B
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 8

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The sulfentate-bombesin (7-14) conjugate has the following
OTHER INFORMATION: molecular structure:
OTHER INFORMATION: p-azidocetatefluorobenzoyl-Gln-Trp-Ala-Val-Gly-His-Leu-Met-NH₂.
US-09-898-887B-1

Query Match 88.0%; Score 22; DB 10; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.2e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH1 8
DB 1 QMAVGH1 7

RESULT 6
US-10-281-840-2
Sequence 2, Application US/10281840
Publication No. US20030082192A1
GENERAL INFORMATION:

APPLICANT: Safavy, Ahmad
TITLE OF INVENTION: Multidrug Multiligand Conjugates for Targeted Drug Delivery
FILE REFERENCE: P6788US01GP
CURRENT APPLICATION NUMBER: US/10/281,840
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US 60/348,299
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-281-840-2

Query Match 88.0%; Score 22; DB 14; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.2e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH1 8
DB 1 QMAVGH1 7

RESULT 7
US-10-341-577-1
Sequence 1, Application US/10341577
Publication No. US20040136906A1
GENERAL INFORMATION:

APPLICANT: Bracco Research U.S.A.
TITLE OF INVENTION: Improved Gastrin Releasing Peptide Compounds
FILE REFERENCE: 57637-1020
CURRENT APPLICATION NUMBER: US/10/341,577
CURRENT FILING DATE: 2003-01-13
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: This peptide is the receptor
OTHER INFORMATION: binding site of bombesin and is also known as BBN[7-14]
US-10-341-577-1

Query Match 88.0%; Score 22; DB 16; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.2e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH1 8
DB 1 QMAVGH1 7

DB 1 QMAVGH1 7

RESULT 8
US-10-004-530A-4
Sequence 4, Application US/10004530A
Publication No. US20030050436A1
GENERAL INFORMATION:

APPLICANT: Coy, David H.
APPLICANT: Moreau, Jacques-Pierre
APPLICANT: Kim, Sun H.
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
FILE REFERENCE: 00537-00900K
CURRENT APPLICATION NUMBER: US/10/004,530A
CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: 09/260,846
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: 08/337,127
PRIOR FILING DATE: 1994-11-10
PRIOR APPLICATION NUMBER: 07/779,039
PRIOR FILING DATE: 1991-10-18
PRIOR APPLICATION NUMBER: 07/502,438
PRIOR FILING DATE: 1990-03-30
PRIOR APPLICATION NUMBER: 07/397,169
PRIOR FILING DATE: 1989-08-21
PRIOR APPLICATION NUMBER: 07/376,555
PRIOR FILING DATE: 1989-07-07
PRIOR APPLICATION NUMBER: 07/317,941
PRIOR FILING DATE: 1989-03-02
PRIOR APPLICATION NUMBER: 07/282,328
PRIOR FILING DATE: 1988-12-09
PRIOR APPLICATION NUMBER: 07/257,998
PRIOR FILING DATE: 1988-10-14
PRIOR APPLICATION NUMBER: 07/248,771
PRIOR FILING DATE: 1988-09-23
Prior application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated peptide
NAME/KEY: VARIANT
LOCATION: 8
OTHER INFORMATION: Xaa = statine
US-10-004-530A-4

Query Match 84.0%; Score 21; DB 14; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.2e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXVXH1 7
DB 1 EQMAVGH1 7

RESULT 9
US-10-182-252A-322
Sequence 322, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUIS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUBMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
FILE REFERENCE: 030307/0205

```
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 322
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-322

Query Match
Best Local Similarity 76.0%; Score 19; DB 12; Length 8;
                33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
Db 1 QIGIPH 6

RESULT 10
US-10-182-252A-940
/ Sequence 940, Application US/10182252A
/ Publication No. US20040072162A1
/ GENERAL INFORMATION:
/ APPLICANT: FOMSGAARD, ANDERS
/ APPLICANT: BRUNAK, SOREN
/ APPLICANT: BUUS, SOREN
/ APPLICANT: CORBET, SYLVIE
/ APPLICANT: LAUEMOLLER, SANNE LISE
/ APPLICANT: HANSEN, JAN
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 940
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-940

Query Match
Best Local Similarity 76.0%; Score 19; DB 12; Length 8;
                33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
Db 1 QIGIPH 6

RESULT 11
US-10-182-252A-941
/ Sequence 941, Application US/10182252A
/ Publication No. US20040072162A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: FOMSGAARD, ANDERS
/ APPLICANT: BRUNAK, SOREN
/ APPLICANT: BUUS, SOREN
/ APPLICANT: CORBET, SYLVIE
/ APPLICANT: LAUEMOLLER, SANNE LISE
/ APPLICANT: HANSEN, JAN
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 941
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-941

Query Match
Best Local Similarity 76.0%; Score 19; DB 12; Length 8;
                33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
Db 1 QIGIPH 6

RESULT 12
US-10-182-252A-942
/ Sequence 942, Application US/10182252A
/ Publication No. US20040072162A1
/ GENERAL INFORMATION:
/ APPLICANT: FOMSGAARD, ANDERS
/ APPLICANT: BRUNAK, SOREN
/ APPLICANT: BUUS, SOREN
/ APPLICANT: CORBET, SYLVIE
/ APPLICANT: LAUEMOLLER, SANNE LISE
/ APPLICANT: HANSEN, JAN
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 942
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-942

Query Match
Best Local Similarity 76.0%; Score 19; DB 12; Length 8;
                33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
```

Db 1 QIGIPH 6

RESULT 13

US-10-182-252A-943

Sequence 943, Application US/10182252A

Publication No. US20040072162A1

GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS

APPLICANT: BRUNAK, SOREN

APPLICANT: BUUS, SOREN

APPLICANT: CORBET, SYLVIE

APPLICANT: LAUEMOLLER, SANNE LISE

APPLICANT: HANSEN, JAN

TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND

FILE REFERENCE: 030307/0205

CURRENT APPLICATION NUMBER: US/10/182,252A

PRIOR FILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: PCT/DK01/00059

PRIOR FILING DATE: 2001-01-29

PRIOR APPLICATION NUMBER: EP 00610017.6

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/179,333

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1388

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 943

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV peptide

US-10-182-252A-943

Query Match 76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
Db 1 QIGIPH 6

RESULT 14

US-10-182-252A-944

Sequence 944, Application US/10182252A

Publication No. US20040072162A1

GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS

APPLICANT: BRUNAK, SOREN

APPLICANT: BUUS, SOREN

APPLICANT: CORBET, SYLVIE

APPLICANT: LAUEMOLLER, SANNE LISE

APPLICANT: HANSEN, JAN

TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND

FILE REFERENCE: 030307/0205

CURRENT APPLICATION NUMBER: US/10/182,252A

PRIOR FILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: PCT/DK01/00059

PRIOR FILING DATE: 2001-01-29

PRIOR APPLICATION NUMBER: EP 00610017.6

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/179,333

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1388

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 944

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV peptide

US-10-182-252A-944

Query Match 76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
Db 1 QIGIPH 6

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-944

Query Match 76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
Db 1 QIGIPH 6

RESULT 15

US-10-182-252A-946

Sequence 946, Application US/10182252A

Publication No. US20040072162A1

GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS

APPLICANT: BRUNAK, SOREN

APPLICANT: BUUS, SOREN

APPLICANT: CORBET, SYLVIE

APPLICANT: LAUEMOLLER, SANNE LISE

APPLICANT: HANSEN, JAN

TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND

FILE REFERENCE: 030307/0205

CURRENT APPLICATION NUMBER: US/10/182,252A

PRIOR FILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: PCT/DK01/00059

PRIOR FILING DATE: 2001-01-29

PRIOR APPLICATION NUMBER: EP 00610017.6

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/179,333

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1388

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 946

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV peptide

US-10-182-252A-946

Query Match 76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
Db 1 QIGIPH 6

RESULT 16

US-10-182-252A-947

Sequence 947, Application US/10182252A

Publication No. US20040072162A1

GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS

APPLICANT: BRUNAK, SOREN

APPLICANT: BUUS, SOREN

APPLICANT: CORBET, SYLVIE

APPLICANT: LAUEMOLLER, SANNE LISE

APPLICANT: HANSEN, JAN

TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND

FILE REFERENCE: 030307/0205

CURRENT APPLICATION NUMBER: US/10/182,252A

PRIOR FILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: PCT/DK01/00059

PRIOR FILING DATE: 2001-01-29

PRIOR APPLICATION NUMBER: EP 00610017.6

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV peptide

US-10-182-252A-947

Query Match 76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 947
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-947
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db       1 QMGIPH 6
```

```
RESULT 17
US-10-182-252A-948
/ Sequence 948, Application US/10182252A
/ Publication No. US20040072162A1
/ GENERAL INFORMATION:
/ APPLICANT: FOMSGAARD, ANDERS
/ APPLICANT: BRUNAK, SOREN
/ APPLICANT: BUNUS, SOREN
/ APPLICANT: COREBT, SYLVIE
/ APPLICANT: LAUEMOLLER, SANNE LISE
/ APPLICANT: HANSEN, JAN
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ PRIOR FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 948
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-948
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db       1 QMGIPH 6
```

```
RESULT 18
US-10-182-252A-950
/ Sequence 950, Application US/10182252A
/ Publication No. US20040072162A1
/ GENERAL INFORMATION:
/ APPLICANT: FOMSGAARD, ANDERS
/ APPLICANT: BRUNAK, SOREN
/ APPLICANT: BUNUS, SOREN
/ APPLICANT: COREBT, SYLVIE
/ APPLICANT: LAUEMOLLER, SANNE LISE
```

```
/ APPLICANT: HANSEN, JAN
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 950
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-950
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db       1 QMGIPH 6
```

```
RESULT 19
US-10-182-252A-951
/ Sequence 951, Application US/10182252A
/ Publication No. US20040072162A1
/ GENERAL INFORMATION:
/ APPLICANT: FOMSGAARD, ANDERS
/ APPLICANT: BRUNAK, SOREN
/ APPLICANT: BUNUS, SOREN
/ APPLICANT: COREBT, SYLVIE
/ APPLICANT: LAUEMOLLER, SANNE LISE
/ APPLICANT: HANSEN, JAN
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 951
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-951
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db       1 QMGIPH 6
```

```
RESULT 20
```

US-10-182-252A-1285
 ; Sequence 1285, Application US/10182252A
 ; Publication No. US20040072162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FOMSGAARD, ANDERS
 ; APPLICANT: BRUNAK, SOREN
 ; APPLICANT: BUS, SOREN
 ; APPLICANT: CORBET, SYLVIE
 ; APPLICANT: LAUEWOLLER, SANNE LISE
 ; APPLICANT: HANSEN, JAN
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
 ; FILE REFERENCE: 030307/0205
 ; CURRENT APPLICATION NUMBER: US/10/182,252A
 ; PRIOR FILING DATE: 2003-04-10
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059
 ; PRIOR FILING DATE: 2001-01-29
 ; PRIOR APPLICATION NUMBER: EP 00610017.6
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US 60/179,333
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1285
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-182-252A-1285

Query Match 76.0%; Score 19; DB 12; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
 Db 1 QLGIPH 6

RESULT 21
 US-10-387-957-6
 ; Sequence 6, Application US/10387957
 ; Publication No. US20040052809A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GlaxoSmithKline Biologicals s.a.
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: B45284
 ; CURRENT APPLICATION NUMBER: US/10/387,957
 ; CURRENT FILING DATE: 2003-03-13
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-387-957-6

Query Match 72.0%; Score 18; DB 12; Length 8;
 Best Local Similarity 28.6%; Pred. No. 1.2e+06;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7
 Db 1 MCGYMKH 7

RESULT 22
 US-10-351-641-1613
 ; Sequence 1613, Application US/10351641
 ; Publication No. US20030186874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Barney, S.
 ; APPLICANT: Guthrie, K.
 ; APPLICANT: Merutka, G.

APPLICANT: Anwer, M.
 ; APPLICANT: Lambert, D.
 ; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
 ; TITLE OF INVENTION: PROPERTIES
 ; FILE REFERENCE: 7872-100
 ; CURRENT APPLICATION NUMBER: US/10/351,641
 ; CURRENT FILING DATE: 2003-01-24
 ; PRIOR APPLICATION NUMBER: 09/350,641
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/315,304
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/082,279
 ; PRIOR FILING DATE: 1998-05-20
 ; NUMBER OF SEQ ID NOS: 1757
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1613
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: HIV-1
 US-10-351-641-1613

Query Match 72.0%; Score 18; DB 14; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.2e+06;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXH 8
 Db 1 WOQMDQHI 8

RESULT 23
 US-10-387-934-6
 ; Sequence 6, Application US/10387934
 ; Publication No. US20040091456A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mettens, Pascal
 ; APPLICANT: Meykens, Rene
 ; APPLICANT: Montevne, Philippe
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: VB60137
 ; CURRENT APPLICATION NUMBER: US/10/387,934
 ; CURRENT FILING DATE: 2003-03-13
 ; PRIOR APPLICATION NUMBER: PCT/EP02/09650
 ; PRIOR FILING DATE: 2002-08-29
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-387-934-6

Query Match 72.0%; Score 18; DB 16; Length 8;
 Best Local Similarity 28.6%; Pred. No. 1.2e+06;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7
 Db 1 MCGYMKH 7

RESULT 24
 US-09-876-904A-181
 ; Sequence 181, Application US/09876904A
 ; Publication No. US20030072794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOULIKAS, TENI
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
 ; AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08

;; PRIOR APPLICATION NUMBER: US 60/210,925
;; PRIOR FILING DATE: 2000-06-09
;; NUMBER OF SEQ ID NOS: 629
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 181
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Karyophilic peptide
US-09-876-904A-181

Query Match 68.0%; Score 17; DB 10; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7
:::|:|
Db 1 HRRKVLH 7

RESULT 25
US-10-387-957-7
; Sequence 7, Application US/10387957
; Publication No. US20040052809A1
; GENERAL INFORMATION:
; APPLICANT: GlaxoSmithKline Biologicals s.a.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45284
; CURRENT APPLICATION NUMBER: US/10/387,957
; CURRENT FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-387-957-7

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7
:::|:|
Db 1 QGYMKH 6

RESULT 26
US-10-014-340-64
; Sequence 64, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patentin Version 3.0
; SEQ ID NO 64
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-64

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 XYXHI 8
:::|:|

Db 1 AVLHV 5

RESULT 27
US-10-182-252A-624
; Sequence 624, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 624
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-624

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 XYXHI 8
:::|:|
Db 1 IICHI 5

RESULT 28
US-10-182-252A-625
; Sequence 625, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 625
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-625

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 XVXHI 8
: : : : :
Db 1 IIGHI 5

RESULT 29
US-10-328-953-94
Sequence 94, Application US/10328953
Publication No. US20040071656A1

GENERAL INFORMATION:
APPLICANT: Wieland, Felix

APPLICANT: Hartl, Franz-Ulrich

TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies

FILE REFERENCE: 11390/46101

CURRENT APPLICATION NUMBER: US/10/328,953

PRIOR FILING DATE: 2002-12-23

PRIOR APPLICATION NUMBER: US 60/342,570

PRIOR FILING DATE: 2001-12-26

PRIOR APPLICATION NUMBER: US 60/343,884

PRIOR FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: US 60/372,620

PRIOR FILING DATE: 2002-04-12

PRIOR APPLICATION NUMBER: US 60/399,342

PRIOR FILING DATE: 2002-07-29

PRIOR APPLICATION NUMBER: US 60/414,834

PRIOR FILING DATE: 2002-09-28

NUMBER OF SEQ ID NOS: 331

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 94

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: peptide in m13 coliphage

US-10-328-953-94

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 XVXHI 8
: : : : :
Db 1 TVQHV 5

RESULT 30
US-10-367-580-186
Sequence 186, Application US/10367580
Publication No. US20040071720A1

GENERAL INFORMATION:
APPLICANT: Rothman, James E.

APPLICANT: Hartl, F. Ulrich

APPLICANT: Hoe, Mee H.

APPLICANT: Houghton, Alan

APPLICANT: Takeuchi, Yoshizumi

APPLICANT: Mayhew, Mark

TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

FILE REFERENCE: 11746/461061

CURRENT APPLICATION NUMBER: US/10/367,580

PRIOR FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: US 09/794,832

PRIOR FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: US 09/011,645

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: PCT/US96/13363

PRIOR FILING DATE: 1996-08-16

PRIOR APPLICATION NUMBER: US 60/002,490
PRIOR FILING DATE: 1995-08-18
PRIOR APPLICATION NUMBER: US 60/002,479
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 349
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 186

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic peptide

US-10-367-580-186

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXVXH 7
: : : : :
Db 1 WRTGVFH 7

RESULT 31
US-10-367-580-234
Sequence 234, Application US/10367580
Publication No. US20040071720A1

GENERAL INFORMATION:
APPLICANT: Rothman, James E.

APPLICANT: Hartl, F. Ulrich

APPLICANT: Hoe, Mee H.

APPLICANT: Houghton, Alan

APPLICANT: Takeuchi, Yoshizumi

APPLICANT: Mayhew, Mark

TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

FILE REFERENCE: 11746/461061

CURRENT APPLICATION NUMBER: US/10/367,580

PRIOR FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: US 09/794,832

PRIOR FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: US 09/011,645

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: PCT/US96/13363

PRIOR FILING DATE: 1996-08-16

PRIOR APPLICATION NUMBER: US 60/002,490

PRIOR FILING DATE: 1995-08-18

PRIOR APPLICATION NUMBER: US 60/002,479

PRIOR FILING DATE: 1995-08-18

NUMBER OF SEQ ID NOS: 349

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 234

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic peptide

US-10-367-580-234

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 16.7%; Pred. No. 1.2e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XVXHI 8
: : : : :
Db 3 QGIRHV 8

RESULT 32
US-10-367-593-186
Sequence 186, Application US/10367593
Publication No. US20040071721A1

GENERAL INFORMATION:
APPLICANT: Rothman, James E.

APPLICANT: Hartl, F. Ulrich

APPLICANT: Hoe, Mee H.

APPLICANT: Houghton, Alan

APPLICANT: Takeuchi, Yoshizumi

APPLICANT: Mayhew, Mark

TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

```
/ APPLICANT: Hartl, F. Ulrich
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Takechi, Yoshizumi
/ APPLICANT: Mayhew, Mark
/ TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
/ FILE REFERENCE: 11746/461012
/ CURRENT APPLICATION NUMBER: US/10/367,593
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: US 09/011,645
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: PCT/US96/13363
/ PRIOR FILING DATE: 1996-08-16
/ PRIOR APPLICATION NUMBER: US 60/002,490
/ PRIOR FILING DATE: 1995-08-18
/ PRIOR APPLICATION NUMBER: US 60/002,479
/ PRIOR FILING DATE: 1995-08-18
/ NUMBER OF SEQ ID NOS: 349
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 186
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-367-593-186
```

```
Query Match      68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 XXXVXH 7
       ::::|:|
Db      1 WRTGVFH 7
```

```
RESULT 33
US-10-367-593-234
/ Sequence 234, Application US/10367593
/ Publication No. US20040071721A1
/ GENERAL INFORMATION:
/ APPLICANT: Rothman, James E.
/ APPLICANT: Hartl, F. Ulrich
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Takechi, Yoshizumi
/ APPLICANT: Mayhew, Mark
/ TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
/ FILE REFERENCE: 11746/461012
/ CURRENT APPLICATION NUMBER: US/10/367,593
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: US 09/011,645
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: PCT/US96/13363
/ PRIOR FILING DATE: 1996-08-16
/ PRIOR APPLICATION NUMBER: US 60/002,490
/ PRIOR FILING DATE: 1995-08-18
/ PRIOR APPLICATION NUMBER: US 60/002,479
/ PRIOR FILING DATE: 1995-08-18
/ NUMBER OF SEQ ID NOS: 349
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 234
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-367-593-234
```

```
Query Match      68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 16.7%; Pred. No. 1.2e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      3 XXVXHI 8
       ::::|:|
Db      3 QGIXHV 8
```

```
RESULT 34
US-10-367-594-186
/ Sequence 186, Application US/10367594
/ Publication No. US20040071722A1
/ GENERAL INFORMATION:
/ APPLICANT: Rothman, James E.
/ APPLICANT: Hartl, F. Ulrich
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Takechi, Yoshizumi
/ APPLICANT: Mayhew, Mark
/ TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
/ FILE REFERENCE: 11746/461041
/ CURRENT APPLICATION NUMBER: US/10/367,594
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: US 09/580,806
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: US 09/011,645
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: PCT/US96/13363
/ PRIOR FILING DATE: 1996-08-16
/ PRIOR APPLICATION NUMBER: US 60/002,490
/ PRIOR FILING DATE: 1995-08-18
/ PRIOR APPLICATION NUMBER: US 60/002,479
/ PRIOR FILING DATE: 1995-08-18
/ NUMBER OF SEQ ID NOS: 349
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 186
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-367-594-186
```

```
Query Match      68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 XXXVXH 7
       ::::|:|
Db      1 WRTGVFH 7
```

```
RESULT 35
US-10-367-594-234
/ Sequence 234, Application US/10367594
/ Publication No. US20040071722A1
/ GENERAL INFORMATION:
/ APPLICANT: Rothman, James E.
/ APPLICANT: Hartl, F. Ulrich
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Takechi, Yoshizumi
/ APPLICANT: Mayhew, Mark
/ TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
/ FILE REFERENCE: 11746/461041
/ CURRENT APPLICATION NUMBER: US/10/367,594
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: US 09/580,806
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: US 09/011,645
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: PCT/US96/13363
/ PRIOR FILING DATE: 1996-08-16
/ PRIOR APPLICATION NUMBER: US 60/002,490
/ PRIOR FILING DATE: 1995-08-18
/ PRIOR APPLICATION NUMBER: US 60/002,479
```

;; PRIOR FILING DATE: 1995-08-18
;; NUMBER OF SEQ ID NOS: 349
;; SOFTWARE: WordPerfect 8.0 for Windows
;; SEQ ID NO 234
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide
US-10-367-594-234

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 16.7%; Pred. No. 1.2e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXHT 8
DB 3 QGIXHV 8

RESULT 36
US-10-367-654-186
;; Sequence 186, Application US/10367654
;; Publication No. US20040071723A1
;; GENERAL INFORMATION:
;; APPLICANT: Rothman, James E.
;; APPLICANT: Hartl, F. Ulrich
;; APPLICANT: Hoe, Mee H.
;; APPLICANT: Houghton, Alan
;; APPLICANT: Takeuchi, Yoshizumi
;; APPLICANT: Mayhew, Mark
;; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
;; FILE REFERENCE: 11746/461032
;; CURRENT APPLICATION NUMBER: US/10/367,654
;; CURRENT FILING DATE: 2003-02-14
;; PRIOR APPLICATION NUMBER: US 10/171,734
;; PRIOR FILING DATE: 2002-06-13
;; PRIOR APPLICATION NUMBER: US 09/636,295
;; PRIOR FILING DATE: 2000-08-10
;; PRIOR APPLICATION NUMBER: US 09/011,645
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: PCT/US96/13363
;; PRIOR FILING DATE: 1996-08-16
;; PRIOR APPLICATION NUMBER: US 60/002,490
;; PRIOR FILING DATE: 1995-08-18
;; PRIOR APPLICATION NUMBER: US 60/002,479
;; PRIOR FILING DATE: 1995-08-18
;; NUMBER OF SEQ ID NOS: 349
;; SOFTWARE: WordPerfect 8.0 for Windows
;; SEQ ID NO 186
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide
US-10-367-654-186

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 XOXVXH 7
DB 1 WRTGVFH 7

RESULT 37
US-10-367-654-234
;; Sequence 234, Application US/10367654
;; Publication No. US20040071723A1
;; GENERAL INFORMATION:
;; APPLICANT: Rothman, James E.
;; APPLICANT: Hartl, F. Ulrich

;; APPLICANT: Hoe, Mee H.
;; APPLICANT: Houghton, Alan
;; APPLICANT: Takeuchi, Yoshizumi
;; APPLICANT: Mayhew, Mark
;; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
;; FILE REFERENCE: 11746/461032
;; CURRENT APPLICATION NUMBER: US/10/367,654
;; CURRENT FILING DATE: 2003-02-14
;; PRIOR APPLICATION NUMBER: US 10/171,734
;; PRIOR FILING DATE: 2002-06-13
;; PRIOR APPLICATION NUMBER: US 09/636,295
;; PRIOR FILING DATE: 2000-08-10
;; PRIOR APPLICATION NUMBER: US 09/011,645
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: PCT/US96/13363
;; PRIOR FILING DATE: 1996-08-16
;; PRIOR APPLICATION NUMBER: US 60/002,490
;; PRIOR FILING DATE: 1995-08-18
;; PRIOR APPLICATION NUMBER: US 60/002,479
;; PRIOR FILING DATE: 1995-08-18
;; NUMBER OF SEQ ID NOS: 349
;; SOFTWARE: WordPerfect 8.0 for Windows
;; SEQ ID NO 234
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide
US-10-367-654-234

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 16.7%; Pred. No. 1.2e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXHT 8
DB 3 QGIXHV 8

RESULT 38
US-10-367-658-186
;; Sequence 186, Application US/10367658
;; Publication No. US20040071724A1
;; GENERAL INFORMATION:
;; APPLICANT: Rothman, James E.
;; APPLICANT: Hartl, F. Ulrich
;; APPLICANT: Hoe, Mee H.
;; APPLICANT: Houghton, Alan
;; APPLICANT: Takeuchi, Yoshizumi
;; APPLICANT: Mayhew, Mark
;; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
;; FILE REFERENCE: 11746/461051
;; CURRENT APPLICATION NUMBER: US/10/367,658
;; CURRENT FILING DATE: 2003-02-14
;; PRIOR APPLICATION NUMBER: US 09/794,529
;; PRIOR FILING DATE: 2001-02-27
;; PRIOR APPLICATION NUMBER: US 09/011,645
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: PCT/US96/13363
;; PRIOR FILING DATE: 1996-08-16
;; PRIOR APPLICATION NUMBER: US 60/002,490
;; PRIOR FILING DATE: 1995-08-18
;; PRIOR APPLICATION NUMBER: US 60/002,479
;; PRIOR FILING DATE: 1995-08-18
;; NUMBER OF SEQ ID NOS: 349
;; SOFTWARE: WordPerfect 8.0 for Windows
;; SEQ ID NO 186
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide
US-10-367-658-186

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXVXVH 7
: : : : :
DB 1 WRTGVFH 7

RESULT 39

US-10-367-658-234
; Sequence 234, Application US/10367658
; Publication No. US20040071724A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461051
; CURRENT APPLICATION NUMBER: US/10/367,658
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,529
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 234
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-658-234

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 16.7%; Pred. No. 1.2e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXVH 8
: : : : :
DB 3 QGIXHV 8

RESULT 40
US-10-367-668-186
; Sequence 186, Application US/10367668
; Publication No. US20040071725A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461072
; CURRENT APPLICATION NUMBER: US/10/367,668
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,517
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 186
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-186

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXVXVH 7
: : : : :
DB 1 WRTGVFH 7

RESULT 41
US-10-367-668-234
; Sequence 234, Application US/10367668
; Publication No. US20040071725A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461072
; CURRENT APPLICATION NUMBER: US/10/367,668
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,517
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 234
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-234

Query Match 68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 16.7%; Pred. No. 1.2e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXVH 8
: : : : :
DB 3 QGIXHV 8

RESULT 42
US-10-139-146-66
; Sequence 66, Application US/10139146
; Publication No. US2003009932A1

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; GENERAL INFORMATION:
; APPLICANT: LORENS, James B.
; TITLE OF INVENTION: RETROVIRAL VECTORS WITH SEPARATION SEQUENCES
; FILE REFERENCE: A-70980/RMS/CYO
; CURRENT APPLICATION NUMBER: US/10/139,146
; CURRENT FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rhesus rat sarcoma virus
; US-10-139-146-66

Query Match      68.0%; Score 17; DB 14; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 XXXXXH 7
       11111
DB      2 GQSLTH 8

RESULT 43
US-10-052-578-13
; Sequence 13, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelii, Quatchek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 13
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
; US-10-052-578-13

Query Match      68.0%; Score 17; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 YXXHI 8
       11111
DB      1 TVQHV 5

RESULT 44
US-10-053-520-13
; Sequence 13, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelii, Quatchek
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; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 13
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
; US-10-053-520-13

Query Match      68.0%; Score 17; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 YXXHI 8
       11111
DB      1 TVQHV 5

RESULT 45
US-10-053-498B-13
; Sequence 13, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelii, Quatchek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 13
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
; US-10-053-498B-13

Query Match      68.0%; Score 17; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 YXXHI 8
       11111
DB      1 TVQHV 5

Search completed: August 19, 2004, 16:00:18
Job time : 38 secs
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